

ME

177157

STIC-Biotech/ChemLib

From: Chernyshev, Olga  
Sent: Friday, January 20, 2006 1:18 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/612,921, sequence search request

Please search SEQ ID NO: 3 down to 95% identity and also 30 contigs of SEQ ID NO: 3 in regular and pending databases.  
Thank you very much!

Olga N. Chernyshev, Ph.D.  
AU 1649  
REM 3C89  
2-0870  
mail 4C70

RECEIVED  
JAN 20 2006  
STIC

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

This Page Blank (22/03/20)

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: January 27, 2006, 18:52:33 ; Search time 3013 Seconds  
(without alignment)  
8829.318 Million cell updates/sec

Title: US-09-612-921B-3

Perfect score: 468

Sequence: 1 atggtcctgagtggtggtggtc.....acttcagcagtggtgactag 468

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl1  
1: gb\_ba:\*  
2: gb\_un:\*  
3: gb\_env:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_str:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_hlg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	100.0	468	6	BD124061
2	468	100.0	468	6	BD263573
3	468	100.0	468	8	AF230377
4	468	100.0	468	11	AY890616
5	468	100.0	1025	6	AR630872
6	468	100.0	1025	6	AX207818
7	468	100.0	1282	6	BD211434
8	468	100.0	1282	6	AR181994
9	468	100.0	1282	6	AR221128
10	468	100.0	1282	6	AR302956
11	468	100.0	1282	6	AF201830
12	468	100.0	1288	6	AF201830
13	468	100.0	2563	6	AX080389
14	468	100.0	2598	6	AX092420
15	468	100.0	2598	6	AX454730
16	468	100.0	2598	6	AX491208
17	468	100.0	2598	8	AY359117
18	468	100.0	2604	8	HSA242738

19	468	100.0	2613	8	HSA242737	AR242737 Homo sapi
20	468	100.0	2648	6	BD211435	BD211435 A novel i
21	468	100.0	2648	6	AR181995	AR181995 Sequence
22	468	100.0	2648	6	AR221129	AR221129 Sequence
23	468	100.0	2648	6	AR302957	AR302957 Sequence
24	468	100.0	2648	6	AX069309	AX069309 Sequence
25	468	100.0	2692	8	BC024747	BC024747 Homo sapi
26	468	100.0	2720	8	AF186094	AF186094 Homo sapi
27	466.4	99.7	468	11	AY893100	AY893100 Synthetic
28	465	99.4	465	6	AX080398	AX080398 Sequence
29	457	97.6	2701	6	CQ722801	CQ722801 Sequence
30	354.4	75.7	480	6	AX675571	AX675571 Sequence
31	351.2	75.0	468	6	AX069335	AX069335 Sequence
32	351.2	75.0	471	9	AF230378	AF230378 Sequence
33	351.2	75.0	1283	9	AF200495	AF200495 Mus muscu
34	351.2	75.0	1284	6	AX080392	AX080392 Sequence
35	351.2	75.0	1284	9	MMU250429	MMU250429 Mus muscu
36	351.2	75.0	1385	6	BD263575	BD263575 IL-1 re
37	350.2	74.8	470	6	BD106430	BD106430 Mammalian
38	348.2	74.4	465	6	AX080399	AX080399 Sequence
39	348.2	74.4	468	6	BD124060	BD124060 DNA and p
40	243	51.9	338	6	BD211432	BD211432 A novel i
41	243	51.9	357	6	AR181992	AR181992 Sequence
42	243	51.9	357	6	AR221126	AR221126 Sequence
43	243	51.9	357	6	AR302954	AR302954 Sequence
44	243	51.9	357	6	AX069304	AX069304 Sequence
45	243	51.9	985	6	BD211433	BD211433 A novel i
46	243	51.9	985	6	AR181993	AR181993 Sequence
47	243	51.9	985	6	AR221127	AR221127 Sequence
48	243	51.9	985	6	AR302955	AR302955 Sequence
49	243	51.9	985	6	AX069305	AX069305 Sequence
50	236	50.4	295	6	BD263574	BD263574 IL-1 re
51	227	48.5	5751	6	BD211436	BD211436 A novel i
52	227	48.5	5751	6	AR181996	AR181996 Sequence
53	227	48.5	5751	6	AR221130	AR221130 Sequence
54	227	48.5	5751	6	AR302958	AR302958 Sequence
55	227	48.5	5751	6	AX069310	AX069310 Sequence
56	227	48.5	6540	6	AX080431	AX080431 Sequence
57	227	48.5	6540	8	HSA271338	AR271338 Homo sapi
58	227	48.5	7604	8	AF216693	AF216693 Homo sapi
59	227	48.5	7605	6	BD211437	BD211437 A novel i
60	227	48.5	7605	6	AR181997	AR181997 Sequence
61	227	48.5	7605	6	AR221131	AR221131 Sequence
62	227	48.5	7605	6	AR302959	AR302959 Sequence
63	227	48.5	7605	6	AX069311	AX069311 Sequence
64	227	48.5	12428	8	AY972853	AY972853 Homo sapi
65	227	48.5	197308	8	AC016724	AC016724 Homo sapi
66	208.6	44.6	382	6	BD263576	BD263576 IL-1 re
67	176.6	37.7	159314	14	AC162860	AC162860 Mus muscu
68	176.6	37.7	199080	14	AC122732	AC122732 Mus muscu
69	176.6	37.7	201610	9	AL732430	AL732430 Mouse DNA
70	174.2	37.2	8032	6	AX069334	AX069334 Sequence
71	162.2	34.7	265773	14	AC106686	AC106686 Rattus no
72	112.8	24.1	550	8	AY182232	AY182232 Macaca fa
73	110.8	23.7	456	6	AX594194	AX594194 Sequence
74	110.8	23.7	534	6	AX594192	AX594192 Sequence
75	110.8	23.7	744	6	AX167150	AX167150 Sequence
76	110.8	23.7	998	6	AR182991	AR182991 Sequence
77	110.8	23.7	998	6	AR182992	AR182992 Sequence
78	110.8	23.7	998	6	AR204382	AR204382 Sequence
79	110.8	23.7	998	6	AR204383	AR204383 Sequence
80	110.8	23.7	998	6	AR207385	AR207385 Sequence
81	110.8	23.7	998	6	AR207386	AR207386 Sequence
82	110.8	23.7	998	6	AX048803	AX048803 Sequence
83	110.8	23.7	998	6	AX048805	AX048805 Sequence
84	110.8	23.7	1008	8	AY029413	AY029413 Homo sapi
85	110.8	23.7	1015	8	AY358846	AY358846 Homo sapi
86	110.8	23.7	1020	6	AX167146	AX167146 Sequence
87	110.8	23.7	1020	6	AX167148	AX167148 Sequence
88	110.2	23.5	462	6	BD135233	BD135233 Sequence
89	110.2	23.5	462	6	BD135232	BD135232 Combinati
90	110.2	23.5	462	6	AR533673	AR533673 Sequence
91	110.2	23.5	474	6	AS0276	AS0276 Sequence 10

92	110.2	23.5	474	6	AR001464	AR001464 Sequence	165	95	20.3	1170	6	AR533682	AR533682 Sequence
93	110.2	23.5	474	6	AR055509	AR055509 Sequence	166	94.2	20.1	574	4	S68977	S68977 gIL-1ra=Int
94	110.2	23.5	474	6	AR085392	AR085392 Sequence	167	93.8	20.0	459	6	AR204390	AR204390 Sequence
95	110.2	23.5	480	11	AY891321	AY891321 Synthetic	168	93.8	20.0	459	6	AX046819	AX046819 Sequence
96	110.2	23.5	480	11	AY891322	AY891322 Synthetic	169	93.8	20.0	459	6	AX071780	AX071780 Sequence
97	110.2	23.5	480	11	BT019664	BT019664 Synthetic	170	93.8	20.0	459	6	AX206847	AX206847 Sequence
98	110.2	23.5	507	11	BT019665	BT019665 Synthetic	171	93.8	20.0	538	9	AY0071844	AY0071844 Mus muscu
99	110.2	23.5	507	6	BD077405	BD077405 Novel pro	172	93.6	20.0	1874	4	AB005148	AB005148 Bos tauru
100	110.2	23.5	514	6	I42450	I42450 Sequence 41	173	92.8	19.8	331	6	AX193645	AX193645 Sequence
101	110.2	23.5	531	6	A49726	A49726 Sequence 1	174	92.8	19.8	553	4	P1GRAP	P1GRAP Sus scrofa
102	110.2	23.5	531	6	A50144	A50144 Sequence 1	175	92.2	19.7	520	9	MUSILRA	M63100 M.musculus
103	110.2	23.5	534	6	AR270658	AR270658 Sequence	176	92.2	19.7	542	9	S64082	S64082 Interleukin
104	110.2	23.5	534	8	HUMILRA	M63099 Human Inter	177	92.2	19.7	604	9	AF001795	AF001795 Mus muscu
105	110.2	23.5	540	6	I09591	I09591 Sequence 1	178	92.2	19.7	1576	6	MUSILRAA	M57555 Mouse Inter
106	110.2	23.5	540	6	I09592	I09592 Sequence 3	179	92.2	19.7	1877	6	E55194	E55194 Interleukin
107	110.2	23.5	543	6	AR004317	AR004317 Sequence	180	92.2	19.7	1877	9	MUSILIN	M74294 Mouse IL-1r
108	110.2	23.5	578	6	CS047660	CS047660 Sequence	181	92.2	19.7	1940	9	MUSILIRA	M64404 Mus domest
109	110.2	23.5	578	6	AR380313	AR380313 Sequence	182	91	19.4	238	6	AX193662	AX193662 Sequence
110	110.2	23.5	578	6	HSILIRAI	X84348 H.sapiens m	183	90.6	19.4	2470	6	BC042532	BC042532 Mus muscu
111	110.2	23.5	579	6	A50279	A50279 Sequence 13	184	89.6	19.1	537	6	AX402017	AX402017 Sequence
112	110.2	23.5	579	6	AR001465	AR001465 Sequence	185	89.6	19.1	537	6	RATILRA	AX402017 Sequence
113	110.2	23.5	579	6	AR055510	AR055510 Sequence	186	89.6	19.1	1938	9	BC070930	BC070930 Rattus no
114	110.2	23.5	600	6	I08135	I08135 Sequence 3	187	88.4	18.9	247	4	AY577820	AY577820 Sus scrof
115	110.2	23.5	600	6	I09594	I09594 Sequence 8	188	87.6	18.7	483	6	AX193585	AX193585 Sequence
116	110.2	23.5	600	6	BD06903	BD06903 Interleuk	189	85.4	18.2	221	4	AF072476	AF072476 Equus cab
117	110.2	23.5	602	6	AR005097	AR005097 Sequence	190	84	17.9	218	6	AX193630	AX193630 Sequence
118	110.2	23.5	602	6	AR036273	AR036273 Sequence	191	82.8	17.7	12565	6	AB4742	AB4742 Sequence 3
119	110.2	23.5	602	6	AR049621	AR049621 Sequence	192	82.8	17.7	12565	6	BD085857	BD085857 Methoda o
120	110.2	23.5	602	6	AR059551	AR059551 Sequence	193	82.8	17.7	12565	6	BD271231	BD271231 Predictio
121	110.2	23.5	602	6	HUMILRAA	M55646 Human iCIL-	194	82.8	17.7	12565	6	CS108085	CS108085 Sequence
122	110.2	23.5	603	6	AR043323	AR043323 Sequence	195	82.8	17.7	12565	6	AR487066	AR487066 Sequence
123	110.2	23.5	603	6	AR103328	AR103328 Sequence	196	82.8	17.7	12565	6	AR493824	AR493824 Sequence
124	110.2	23.5	717	6	I42449	I42449 Sequence 40	197	82.8	17.7	12565	6	AR542767	AR542767 Sequence
125	110.2	23.5	777	6	CS047661	CS047661 Sequence	198	82.8	17.7	12565	6	AX052807	AX052807 Sequence
126	110.2	23.5	777	8	AF043143	AF043143 Homo sapi	199	82.8	17.7	12565	6	AX067267	AX067267 Sequence
127	110.2	23.5	1684	8	HSILIRAP	X53296 H.sapiens m	200	82.8	17.7	12565	8	AX067267	AX067267 Sequence
128	110.2	23.5	1740	6	CO861652	CO861652 Sequence	201	82.8	17.7	12565	6	HSILIRECA	X64532 H.sapiens g
129	110.2	23.5	1740	8	HSILIRA	X52015 H.sapiens m	202	82.8	17.7	12565	8	AY196903	AY196903 Homo sapi
130	110.2	23.5	1742	6	CS047655	CS047655 Sequence	203	82.8	17.7	13414	8	HSU65590	HSU65590 Homo sapien
131	110.2	23.5	1802	6	CS033142	CS033142 Sequence	204	82.8	17.7	70869	14	AC111146	AC111146 Homo sapi
132	110.2	23.5	1802	6	CS042094	CS042094 Sequence	205	82.8	17.7	737	10	BV211058	BV211058 Homo sapi
133	110.2	23.5	1802	6	CS047662	CS047662 Sequence	206	82.4	15.9	92799	14	AC135817	AC135817 Rattus no
134	110.2	23.5	1927	6	AX281640	AX281640 Sequence	207	74.6	15.2	6350	6	BD087375	BD087375 Transgeni
135	110.2	23.5	1927	6	CS118896	CS118896 Sequence	208	71.2	15.2	6350	6	E55205	E55205 Interleukin
136	110.2	23.5	2148	8	BC068441	BC068441 Homo sapi	209	71.2	15.2	6350	9	MUSILIRN	AX003692 Sequence
137	110.2	23.3	459	6	AX206836	AX206836 Sequence	210	71.2	15.2	6350	6	AX003692	AX003692 Sequence
138	109.2	23.3	1366	6	AR204387	AR204387 Sequence	211	71.2	15.2	6350	9	MUSILIRN	AX003692 Sequence
139	109.2	23.3	1366	6	AR204387	AR204387 Sequence	212	71.2	15.2	16645	9	ALU732528	ALU732528
140	109.2	23.3	1366	6	AR207389	AR207389 Sequence	213	71.2	15.2	177551	14	AC099634	AC099634 Mus muscu
141	109.2	23.3	1366	6	AR207389	AR207389 Sequence	214	70.2	15.0	5445	6	AR204388	AR204388 Sequence
142	109.2	23.3	1366	6	AX048814	AX048814 Sequence	215	70.2	15.0	5445	6	AX048817	AX048817 Sequence
143	109.2	23.3	1366	6	AX048816	AX048816 Sequence	216	70.2	15.0	5445	8	AF334756	AF334756 Homo sapi
144	109.2	23.3	1366	6	AF334755	AF334755 Homo sapi	217	70.2	15.0	7660	6	AX594195	AX594195 Sequence
145	108.6	23.2	1707	8	BC009745	BC009745 Homo sapi	218	70.2	15.0	11129	8	AY972854	AY972854 Homo sapi
146	108.6	23.2	1716	6	CO981297	CO981297 Homo sapi	219	66.4	14.2	215	6	AX193628	AX193628 Sequence
147	108.6	23.2	1693	6	AB038268	AB038268 Tursiops	220	64.6	13.8	4388	6	AR204389	AR204389 Sequence
148	104	22.2	1693	6	AX206834	AX206834 Sequence	221	64.6	13.8	4388	6	AX048818	AX048818 Sequence
149	103	22.0	1036	4	AY026462	AY026462 Canis fam	222	64.6	13.0	13017	6	AX167182	AX167182 Sequence
150	97.6	20.9	563	4	AF216526	AF216526 Canis fam	223	60.8	13.0	472	6	CO722803	CO722803 Sequence
151	96	20.5	1594	4	RAB1IRAI	D21832 Oryctolagus	224	60.8	13.0	474	6	BD077406	BD077406 Novel pro
152	95.8	20.5	1612	4	CS047651	CS047651 Sequence	225	60.8	13.0	477	6	BD224186	BD224186 Human IL-
153	95.8	20.5	2991	6	CS047649	CS047649 Sequence	226	60.8	13.0	477	6	BD224187	BD224187 Human IL-
154	95.6	20.4	3121	6	CS047649	CS047649 Sequence	227	60.8	13.0	477	6	AR629781	AR629781 Sequence
155	95.6	20.4	3121	6	CS047649	CS047649 Sequence	228	60.8	13.0	477	8	AF201831	AF201831 Homo sapi
156	95.4	20.4	603	6	AX127225	AX127225 Sequence	229	60.8	13.0	819	6	CS071287	CS071287 Sequence
157	95.4	20.4	1590	6	DB3714	DB3714 Equus cabal	230	56.6	12.1	764	10	BV209309	BV209309 IL1F10_33
158	95.4	20.4	1590	6	ECU92482	ECU92482 Equus cabal	231	54.2	11.6	662	5	CR390593	CR390593 Gallus ga
159	95.4	20.4	1614	4	AX127224	AX127224 Sequence	232	52.8	11.3	329	6	AX193643	AX193643 Sequence
160	95.4	20.4	1614	4	AX127224	AX127224 Sequence	233	52.8	11.3	520	6	AX193587	AX193587 Sequence
161	95.4	20.3	167423	14	AC145359	AC145359 Macropus	234	52.8	11.3	563	6	CO722804	CO722804 Sequence
162	95.2	20.3	475	6	AR533674	AR533674 Sequence	235	52.8	11.3	585	6	AR560137	AR560137 Sequence
163	95	20.3	1167	6	AR533683	AR533683 Sequence	236	52.8	11.3	585	6	AX052581	AX052581 Sequence
164	95	20.3	1167	6	AR533683	AR533683 Sequence	237	52.8	11.3	585	6	AX052581	AX052581 Sequence

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN
BD124061.1	GI:23219006	JP 200250046-A/2.	Homo sapiens (human)							
			Homo sapiens							
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.							
			1 (bases 1 to 468)							
			Stma.J.F.							
			DNA and polypeptide of IL-1-delta							
			Patent: JP 200250046-A 2 08-JAN-2002;							
			IMMUNEX CORP							
			OS Homo sapiens (human)							
			PN JP 200250046-A/2							
			PD 08-JAN-2002							
			PF 08-JAN-1999 JP 2000527652							
			PR 09-JAN-1998 US 60/071074.01-JUN-1998 US 60/087393 PR							
			JOHN ERNEST SIMS							
			PC C12N15/09,C07K14/545,C07K16/24,C12N1/19,C12N1/21,C12N5/10, PC							
			C12P21/08//							
			PC C12M1/00,C12N15/00,C12N5/00							
			CC DNA and polypeptide of IL-1-delta							
			PH Key							
			FT source							
			1..468							
			/organism="Homo sapiens (human)".							
			Location/Qualifiers							
			1..468							
			/organism="Homo sapiens"							
			/mol_type="genomic DNA"							
			/db_xref="taxon:9606"							
Query Match	100.0%;	Score 468;	DB 6;	Length 468;						
Best Local Similarity	100.0%;	Pred. No. 1.9e-107;								
Matches 468;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;						
QY	1	ATGTCCTGATGAGGGGGCGCTGTGCTTCCGAAATGAAGACCTCGCATTTGAAGTCCTTAT	60							
DB	1	ATGTCCTGATGAGGGGGCGCTGTGCTTCCGAAATGAAGACCTCGCATTTGAAGTCCTTAT	60							
QY	61	CTGCATATATACCAAGCTTTCTAGCTGAGAGGCTGCATGACAGGAAGTCATTAAAGTGAA	120							
DB	61	CTGCATATATACCAAGCTTTCTAGCTGAGAGGCTGCATGACAGGAAGTCATTAAAGTGAA	120							
QY	121	GAGATCAGCGTGTGCCCAATCGGTGGCTGGATGCCAGCCTGTCCCGGTCATCTGGGT	180							
DB	121	GAGATCAGCGTGTGCCCAATCGGTGGCTGGATGCCAGCCTGTCCCGGTCATCTGGGT	180							
QY	181	GTCAGAGGTGGAAGCCAGTGCCTGTCTATGTGGGGTGGGGCAGAGAGCCGACTTTAAACTTA	240							
DB	181	GTCAGAGGTGGAAGCCAGTGCCTGTCTATGTGGGGTGGGGCAGAGAGCCGACTTTAAACTTA	240							
QY	241	GAGCAGTGAACATCATGTGAGCTCTATCTTGGTGCCAAAGATTCAGAGACTTCACTTC	300							
DB	241	GAGCAGTGAACATCATGTGAGCTCTATCTTGGTGCCAAAGATTCAGAGACTTCACTTC	300							
QY	301	TACCGGCGGACATGAGGCTCACTTCAGCTTGAAGTGGCTGCTTACCGGAGCTGTTTC	360							
DB	301	TACCGGCGGACATGAGGCTCACTTCAGCTTGAAGTGGCTGCTTACCGGAGCTGTTTC	360							
QY	361	CTGTGACAGGTGTGCTTGAAGCCGATCAGCTGTCTGAGACTACCAAGCTTCCCGAAGATGT	420							
DB	361	CTGTGACAGGTGTGCTTGAAGCCGATCAGCTGTCTGAGACTACCAAGCTTCCCGAAGATGT	420							

ACCESSION BD63573.1 GI:33073341  
VERSION BD63573.1  
KEYWORDS UP 2002533122-A/7.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo;  
REFERENCE 1 (bases 1 to 468)  
AUTHORS Goddard, A. and Pan, J.  
TITLE IL-1 related polypeptides  
JOURNAL Patent: JP 2002533122-A 2.08-OCT-2002;  
GENENTECH INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002533122-A/7  
PD 08-OCT-2002  
PF 22-DEC-1998 JP 2000591188  
PR (23-DEC-1998 US) 60/113430, 22-JAN-1999 US 60/116843 PR  
13-APR-1999 US 60/129122  
PI AUDREY GODDARD, JAMES PAN  
PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12N15/00, C12N5/00  
CC IL-1 related polypeptides  
FH Key . Location/Qualifiers  
FT source 1..468  
FT Location/Qualifiers  
1..468  
/organism="Homo sapiens (human)".  
FEATURES  
source  
1..468  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 100.0%; Score 468; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.9e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGTCTGAGTGGGGGCGTGTCTCCGAAATGAAGAAGCTGGATTGAAGTCTTAT 60  
DB 1 ATGGTCTGAGTGGGGGCGTGTCTCCGAAATGAAGAAGCTGGATTGAAGTCTTAT 60  
QY 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGAGATCAATTAAGTGA 120  
DB 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGAGATCAATTAAGTGA 120  
QY 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCGACGCTGTCCCGTCACTGGGT 180  
DB 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCGACGCTGTCCCGTCACTGGGT 180  
QY 181 GTCCAGGCTGGAAGCCAGTGTCTGCAATGTTGGGGTGGGGGAGAGCCGACTTAACACTA 240  
DB 181 GTCCAGGCTGGAAGCCAGTGTCTGCAATGTTGGGGTGGGGGAGAGCCGACTTAACACTA 240  
QY 241 GAGCAGTGAACATCATGAGACTTATCTTGGTGCAGAGATCAAGAGCTTCACTTC 300  
DB 241 GAGCAGTGAACATCATGAGACTTATCTTGGTGCAGAGATCAAGAGCTTCACTTC 300  
QY 301 TACCGGCGGGAATGAGGCTCACTCCAGCTTCAAGTGTGCTGCTTACCCGGGCTGGTTC 360  
DB 301 TACCGGCGGGAATGAGGCTCACTCCAGCTTCAAGTGTGCTGCTTACCCGGGCTGGTTC 360  
QY 361 CTGTGACGCGTGTGAGAGCGGATGAGCTGTGCAAGCTCAAGAGCTTCCGAGAAATGGT 420  
DB 361 CTGTGACGCGTGTGAGAGCGGATGAGCTGTGCAAGCTCAAGAGCTTCCGAGAAATGGT 420  
QY 421 GGCTGGAATGCCCATCATCAGACTTCACTTCCAGCAGTGTGACTAG 468  
DB 421 GGCTGGAATGCCCATCATCAGACTTCACTTCCAGCAGTGTGACTAG 468

LOCUS AF230377 468 bp mRNA linear PRI 01-NOV-2001  
DEFINITION Homo sapiens interleukin-1 delta mRNA, complete cds.  
ACCESSION AF230377  
VERSION AF230377.1 GI:9651788  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo;  
REFERENCE 1 (bases 1 to 468)  
AUTHORS Debets, R., Timans, J.C., Homey, B., Zurawski, S., Sana, T.R., Lo, S.,  
Wagner, J., Edwards, G., Clifford, T., Menon, S., Bazan, J.F. and  
Kastelein, R.A.  
TITLE Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,  
function as an antagonist and agonist of NF-kappa B activation  
through the orphan IL-1 receptor-related protein 2  
JOURNAL J. Immunol. 167 (3), 1440-1446 (2001)  
1146363  
2 (bases 1 to 468)  
Kastelein, R.A., Timans, J.C., Sana, T., Debets, R. and Bazan, F.  
REFERENCE Direct Submission Molecular Biology, DNAX Research Institute,  
Submitted (01-FEB-2000) 901 California Ave, Palo Alto, CA 94304, USA  
JOURNAL Location/Qualifiers  
TITLE  
AUTHORS  
COMMENT  
FEATURES  
source  
1..468  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/map="2q"  
1..468  
/note="IL-1delta; cytokine"  
/codon\_start=1  
/product="interleukin-1 delta"  
/protein\_id="AF91274.1"  
/db\_xref="GI:9651789"  
/translation="MVLGSLCPRMKDSALKVLYLHNNQLIAGGLHAKYIKGEISV  
VPRWIDASPVILGVGSGSGLSCVGEPTLPEVNIEMELYLAKSKSSTFVR  
RDMGLTSSPESAVPGMFLCTVPEADQPVRLTLPENGMNAPIITDYPFGCD"  
ORIGIN  
Query Match 100.0%; Score 468; DB 8; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.9e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGTCTGAGTGGGGGCGTGTCTCCGAAATGAAGAAGCTGGATTGAAGTCTTAT 60  
DB 1 ATGGTCTGAGTGGGGGCGTGTCTCCGAAATGAAGAAGCTGGATTGAAGTCTTAT 60  
QY 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGAGATCAATTAAGTGA 120  
DB 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGAGATCAATTAAGTGA 120  
QY 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCGACGCTGTCCCGTCACTGGGT 180  
DB 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCGACGCTGTCCCGTCACTGGGT 180  
QY 181 GTCCAGGCTGGAAGCCAGTGTCTGCAATGTTGGGGTGGGGGAGAGCCGACTTAACACTA 240  
DB 181 GTCCAGGCTGGAAGCCAGTGTCTGCAATGTTGGGGTGGGGGAGAGCCGACTTAACACTA 240  
QY 241 GAGCAGTGAACATCATGAGACTTATCTTGGTGCAGAGATCAAGAGCTTCACTTC 300  
DB 241 GAGCAGTGAACATCATGAGACTTATCTTGGTGCAGAGATCAAGAGCTTCACTTC 300  
QY 301 TACCGGCGGGAATGAGGCTCACTCCAGCTTCAAGTGTGCTGCTTACCCGGGCTGGTTC 360  
DB 301 TACCGGCGGGAATGAGGCTCACTCCAGCTTCAAGTGTGCTGCTTACCCGGGCTGGTTC 360  
QY 361 CTGTGACGCGTGTGAGAGCGGATGAGCTGTGCAAGCTCAAGAGCTTCCGAGAAATGGT 420  
DB 361 CTGTGACGCGTGTGAGAGCGGATGAGCTGTGCAAGCTCAAGAGCTTCCGAGAAATGGT 420

**RESULT 4**  
**AY890616**  
**LOCUS** AY890616 468 bp mRNA linear SYN 29-MAR-2005  
**DEFINITION** Synthetic construct Homo sapiens clone FHL41295.01x interleukin-1 family member 5 (IL1F5) mRNA, complete cds.  
**ACCESSION** AY890616  
**VERSION** AY890616.1 GI:61364535  
**KEYWORDS** Human ORF project.  
**SOURCE** synthetic construct  
**ORGANISM** other sequences; artificial sequences.  
**REFERENCE** 1 (bases 1 to 468)  
**AUTHORS** Hines, L., Rolfs, A., Jepsen, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Kundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.  
**TITLE** Cloning of human full-length CDS in Creator (TM) recombinational vector system  
**COMMENT** 2 (bases 1 to 468)  
**JOURNAL** Hines, L., Rolfs, A., Jepsen, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Kundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.  
**REFERENCE** Direct Submission  
**AUTHORS** Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard-Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA  
**TITLE** This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Fusion(TM) cloning system. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.  
**FEATURES**  
**Source**  
1..468  
/organism="synthetic construct"  
/mol\_type="mRNA"  
/db\_xref="taxon:32630"  
/clone="FHL41295.01x"  
/lab\_host="Escherichia coli DH5alpha T1 resistant"  
/notes="derived from MGC template"  
1..468  
/gene="IL1F5"  
1..468  
/gene="IL1F5"  
/notes="delta"  
/codon\_start=1  
/translation\_table=11  
/product="interleukin 1 family member 5"  
/protein\_id="AAK42558.1"  
/db\_xref="GI:61364535"  
/translation="MVLSGALCFPRKDSALKVLYLHNNQLAGLHAGKVIKGEISIVRNRLDLSIPVIGVGSGCSCGSGDEPITLIEVNIWEIYLAKESKSTFYRVDWGLTSSFEBAAYPGWFLCTVPEADQPLRLTPENGMNAPITDFYPOOD"  
**ORIGIN**  
Query Match 100.0%; Score 468; DB 11; Length 468;  
Query Local Similarity 100.0%; Pred. No. 1.9e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 ATGCTCTAGTGGGCGCTGCTTCGGAATGAAGACCTCGCATTTGAAGTCTTTAT 60  
2 ATGCTCTAGTGGGCGCTGCTTCGGAATGAAGACCTCGCATTTGAAGTCTTTAT 60  
3 CTGCATATTACCACTTCTAGCTGAGAGGCTGCATGCAGGAAGTCAATTAAAGTAA 120

[illegible]

```

Db      358 TACCGGGGAGCATTGGGGCTCACCAGCTTGAGTGGGTGCTACCGGGGTGTTTC 417
Qy      361 CTGTGACGGTGCCTGAAGCCGATCAGCTGTGACTCAACCCAGCTTCCGAGATGT 420
Db      418 CTGTGACGGTGCCTGAAGCCGATCAGCTGTGACTCAACCCAGCTTCCGAGATGT 477
Qy      421 GGCTGGAATGCCCATCAGACTTCTACTCCAGAGTGTGACTAG 468
Db      478 GGCTGGAATGCCCATCAGACTTCTACTCCAGAGTGTGACTAG 525

RESULT 6
LOCUS   AX207818 1025 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 1 from Patent WO0157219.
ACCESSION AX207818
VERSION   AX207818.1 GI:15422465
KEYWORDS
SOURCE   unidentified
ORGANISM unidentified
          unclassified sequences.
REFERENCE
  1 Debeets,J.E., Timans,J.C., Bazan,J.F. and Kastelein,R.A.
    Mammalian interleukin-1-delta and -epsilon. Their use in
    therapeutic and diagnostic methods.
    Patent: WO 0157219-A 1 09-AUG-2001;
    SCHERING CORPORATION (US)
FEATURES
  source
    1..1025
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"
    /note="Description of Unknown Organism: primate; surmised
    Homo sapiens"
    58..525
    /note="unnamed protein product"
    /codon_start=1
    /protein_id="CAC60372.1"
    /db_xref="GI:15422465"
    /translation="MVLISGALCFPMKDSALKVLYLHNNQLIAGGLHAGKVIKGEISV
    VPRMWDASLSPVILGVGSGQCLSCGVGEPITLPRVIMELYLKAKSKSTFPR
    RMDGLTSSFESAAYPMFLCTVPEADQPVRLTQLPENGWNNAPITDVFQCD"

ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 1025;
Best Local Similarity 100.0%; Pred. No. 1,8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGCTCTGAGTGGGGGCGCTGTGCTCCGAATGAAGGACTCGGCAATTGAAGTCTTAT 60
Db      58 ATGGCTCTGAGTGGGGGCGCTGTGCTCCGAATGAAGGACTCGGCAATTGAAGTCTTAT 117
Qy      61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGGTGAA 120
Db      118 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGGTGAA 177
Qy      121 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTCAATCTGGGT 180
Db      121 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTCAATCTGGGT 237
Qy      178 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTCAATCTGGGT 237
Db      181 GTCCAGGGTGAAGCAGATGCTGTGATGTGGGGTGGGGGAGAGCCGACTCTTAACACTA 240
Qy      238 GTCCAGGGTGAAGCAGATGCTGTGATGTGGGGTGGGGGAGAGCCGACTCTTAACACTA 297
Db      241 GAGCAGGTGAACATCATGAGACTCTATCTTGGTGGCAAGAAATCCAAGAGCTTCACTTC 300
Qy      298 GAGCAGGTGAACATCATGAGACTCTATCTTGGTGGCAAGAAATCCAAGAGCTTCACTTC 357
Db      301 TACCGGGGAGCATTGGGGCTCACCAGCTTCAAGTGGGTGGTCAACCGGGGTGTTTC 360
Qy      358 TACCGGGGAGCATTGGGGCTCACCAGCTTCAAGTGGGTGGTCAACCGGGGTGTTTC 417

```

```

Qy      361 CTGTGACGGTGCCTGAAGCCGATCAGCTGTGACTCAACCCAGCTTCCGAGATGT 420
Db      418 CTGTGACGGTGCCTGAAGCCGATCAGCTGTGACTCAACCCAGCTTCCGAGATGT 477
Qy      421 GGCTGGAATGCCCATCAGACTTCTACTCCAGAGTGTGACTAG 468
Db      478 GGCTGGAATGCCCATCAGACTTCTACTCCAGAGTGTGACTAG 525

RESULT 7
LOCUS   BD211434 1282 bp DNA linear PAT 17-JUL-2003
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
ACCESSION BD211434
VERSION   BD211434.1 GI:33021204
KEYWORDS JP 2002510492-A/3.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo.
REFERENCE
  1 (bases 1 to 1282)
  Ford,J. and Pace,A.
  A novel interleukin-1 receptor antagonist and uses thereof
  Patent: JP 2002510492-A 3 09-APR-2002;
  HYSQ INC
COMMENT
  OS Homo sapiens (human)
  PN JP 2002510492-A/3
  PD 09-APR-2002
  PF 05-APR-1998 JP 2000542457
  PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR
  20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR
  31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR
  17-FEB-1999 US 09/251370
  PI JOHN FORD, ANN PACE
  PC C12N15/09,A61K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,
  PC C12N1/19,
  PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC
  C12N15/00,
  PC A61K37/02,C12N5/00
  CC A novel interleukin-1 receptor antagonist and uses thereof FH
  Key Location/Qualifiers
  FT source 1..1282
    Location/Qualifiers
    1..1282
    /organism="Homo sapiens (human)"
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 468; DB 6; Length 1282;
Best Local Similarity 100.0%; Pred. No. 1,8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGCTCTGAGTGGGGGCGCTGTGCTCCGAATGAAGGACTCGGCAATTGAAGTCTTAT 60
Db      73 ATGGCTCTGAGTGGGGGCGCTGTGCTCCGAATGAAGGACTCGGCAATTGAAGTCTTAT 132
Qy      121 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTCAATCTGGGT 180
Db      121 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTCAATCTGGGT 252
Qy      178 GAGATCAGCGTGGTCCCAATCGGTGGTGGATGCCAGCTGTCCCCCGTCAATCTGGGT 252
Db      181 GTCCAGGGTGAAGCAGATGCTGTGATGTGGGGTGGGGGAGAGCCGACTCTTAACACTA 240
Qy      253 GTCCAGGGTGAAGCAGATGCTGTGATGTGGGGTGGGGGAGAGCCGACTCTTAACACTA 312
Db      241 GAGCAGGTGAACATCATGAGACTCTATCTTGGTGGCAAGAAATCCAAGAGCTTCACTTC 300

```



Db 313 GAGCAGTGAATCATATGAGCTCTATCTGTGTCAGGAATCCAGAGCTTCACTTC 372  
Qy 301 TACCGGGGGGACATGGGGGCTCACTCCAGCTTCCAGTGGCTGCTACCCGGGCTGGTTC 360  
Db 373 TACCGGGGGGACATGGGGGCTCACTCCAGCTTCCAGTGGCTGCTACCCGGGCTGGTTC 432  
Qy 361 CTGTGACAGCGTCTGTAAGCCGATCAGCTGTCAAGACTCAACCCAGCTTCCGAGATGGT 420  
Db 433 CTGTGACAGCGTCTGTAAGCCGATCAGCTGTCAAGACTCAACCCAGCTTCCGAGATGGT 492  
Qy 421 GGCTGAATGCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 468  
Db 493 GGCTGAATGCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 540

RESULT 8  
AR181994 1282 bp DNA linear PAT 20-APR-2002  
LOCUS AR181994  
DEFINITION Sequence 4 from patent US 6337072.  
ACCESSION AR181994  
VERSION AR181994.1 GI:20224910  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1282)  
AUTHORS Ford, J. and Pace, A.  
TITLE Interleukin-1 receptor antagonist and recombinant production thereof  
JOURNAL Patent: US 6337072-A 4 08-JAN-2002;  
FEATURES Location/Qualifiers  
source 1..1282  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 468; DB 6; Length 1282;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTGGGATTTGAGTCTTTAT 60  
Db 73 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTGGGATTTGAGTCTTTAT 132  
Qy 61 CTGATATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTATTAAAGTGA 120  
Db 133 CTGATATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTATTAAAGTGA 192  
Qy 121 GAGATCAGCGTGTGCTCCCAATCGGTGGTGGATGACAGCTGTCCCGCTGATCTGGGT 180  
Db 193 GAGATCAGCGTGTGCTCCCAATCGGTGGTGGATGACAGCTGTCCCGCTGATCTGGGT 252  
Qy 181 GTCCAGGGTGAAGCCAGTGTCTGTATGTGGGGTGGGAGAGCCGACTTAAACTA 240  
Db 253 GTCCAGGGTGAAGCCAGTGTCTGTATGTGGGGTGGGAGAGCCGACTTAAACTA 312  
Qy 241 GAGCAGTGAACATCATGAGACTCTATTGTGTCCAGAGAACTCAAGACTTCACTTC 300  
Db 313 GAGCAGTGAACATCATGAGACTCTATTGTGTGTCCAGAGAACTCAAGACTTCACTTC 372  
Qy 301 TACCGGGGGGACATGGGGGCTCACTCCAGCTTCCAGTGGCTGACCCGGGCTGGTTC 360  
Db 373 TACCGGGGGGACATGGGGGCTCACTCCAGCTTCCAGTGGCTGACCCGGGCTGGTTC 432  
Qy 361 CTGTGACAGCGTCTGTAAGCCGATCAGCTGTCAAGACTCAACCCAGCTTCCGAGATGGT 420  
Db 433 CTGTGACAGCGTCTGTAAGCCGATCAGCTGTCAAGACTCAACCCAGCTTCCGAGATGGT 492  
Qy 421 GGCTGAATGCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 468  
Db 493 GGCTGAATGCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 540

RESULT 9  
AR221128 1282 bp DNA linear PAT 26-SEP-2002  
LOCUS AR221128  
DEFINITION Sequence 4 from patent US 6426191.  
ACCESSION AR221128  
VERSION AR221128.1 GI:23328013  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1282)  
AUTHORS Ford, J. and Pace, A.  
TITLE Assays involving an IL-1 receptor antagonist  
JOURNAL Patent: US 6426191-A 4 30-JUL-2002;  
FEATURES Location/Qualifiers  
source 1..1282  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 100.0%; Score 468; DB 6; Length 1282;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTGGGATTTGAGTCTTTAT 60  
Db 73 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTGGGATTTGAGTCTTTAT 132  
Qy 61 CTGATATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTATTAAAGTGA 120  
Db 133 CTGATATATTAACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTATTAAAGTGA 192  
Qy 121 GAGATCAGCGTGTGCTCCCAATCGGTGGTGGATGACAGCTGTCCCGCTGATCTGGGT 180  
Db 193 GAGATCAGCGTGTGCTCCCAATCGGTGGTGGATGACAGCTGTCCCGCTGATCTGGGT 252  
Qy 181 GTCCAGGGTGAAGCCAGTGTCTGTATGTGGGGTGGGAGAGCCGACTTAAACTA 240  
Db 253 GTCCAGGGTGAAGCCAGTGTCTGTATGTGGGGTGGGAGAGCCGACTTAAACTA 312  
Qy 241 GAGCAGTGAACATCATGAGACTCTATTGTGTCCAGAGAACTCAAGAGCTTCACTTC 300  
Db 313 GAGCAGTGAACATCATGAGACTCTATTGTGTGTCCAGAGAACTCAAGAGCTTCACTTC 372  
Qy 301 TACCGGGGGGACATGGGGGCTCACTCCAGCTTCCAGTGGCTGACCCGGGCTGGTTC 360  
Db 373 TACCGGGGGGACATGGGGGCTCACTCCAGCTTCCAGTGGCTGACCCGGGCTGGTTC 432  
Qy 361 CTGTGACAGCGTCTGTAAGCCGATCAGCTGTCAAGACTCAACCCAGCTTCCGAGATGGT 420  
Db 433 CTGTGACAGCGTCTGTAAGCCGATCAGCTGTCAAGACTCAACCCAGCTTCCGAGATGGT 492  
Qy 421 GGCTGAATGCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 468  
Db 493 GGCTGAATGCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 540

RESULT 10  
AR302956 1282 bp DNA linear PAT 12-JUN-2003  
LOCUS AR302956  
DEFINITION Sequence 4 from patent US 6541623.  
ACCESSION AR302956  
VERSION AR302956.1 GI:31691556  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1282)  
AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.  
TITLE Interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: US 6541623-A 4 01-APR-2003;  
Hyseq, Inc.; Sunnyvale, CA

FEATURES  
source Location/Qualifiers  
1..1282  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 1282;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGGACTCGGCAATGAAGTGCCTTTAT 60  
DB 73 ATGGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGGACTCGGCAATGAAGTGCCTTTAT 132  
QY 61 CTGCAATTAATACCAAGCTTCTAGCTGAGAGGCTGATGACAGGAAAGTCAATTAAGGTGAA 120  
DB 133 CTGCAATTAATACCAAGCTTCTAGCTGAGAGGCTGATGACAGGAAAGTCAATTAAGGTGAA 192  
QY 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGATGACAGCTGTCCCGTCACTCGGCT 180  
DB 193 GAGATCAGCGTGTGCTCCCAATCGGTGAGATGACAGCTGTCCCGTCACTCGGCT 252  
QY 181 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGTGGGGCAGAGCCGACTTAACACTA 240  
DB 253 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGTGGGGCAGAGCCGACTTAACACTA 312  
QY 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCCAGGAATCCAGAGCTTCACTTC 300  
DB 313 GAGCAGTGAACATCATGAGCTTATCTTGTGTCCAGGAATCCAGAGCTTCACTTC 372  
QY 301 TACCGGGGGGACATGGGGCTTCACTCGAGCTTCCAGTGGGTGCTTCCCGGCTGTTTC 360  
DB 373 TACCGGGGGGACATGGGGCTTCACTCGAGCTTCCAGTGGGTGCTTCCCGGCTGTTTC 432  
QY 361 CTGTGACGCGTGTCTGAGAGCCGATGACCTGTGACACTCACCCAGCTTCCGAGATGCT 420  
DB 433 CTGTGACGCGTGTCTGAGAGCCGATGACCTGTGACACTCACCCAGCTTCCGAGATGCT 492  
QY 421 GGCTGGAATGCCCATCAGACTTCTACTTCCAGAGGTGACTAG 468  
DB 493 GGCTGGAATGCCCATCAGACTTCTACTTCCAGAGGTGACTAG 540

## RESULT 11

AX069307 1282 bp DNA linear PAT 25-JAN-2001  
LOCUS AX069307  
DEFINITION Sequence 4 from Patent WO0102571.  
ACCESSION AX069307  
VERSION AX069307.1 GI:12579179  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Ford, J. and Pace, A.  
TITLE A interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: WO 0102571-A 4 11-JAN-2001;  
JOURNAL HYSEQ, INC. (US)  
FEATURES Location/Qualifiers  
source 1..1282  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
73..540  
/note="unassigned protein product"  
/codon\_start=1  
/protein\_id="CAC27298.1"  
/db\_xref="GI:12579180"  
/translation="MVLGALCFPMKDSALKVLIHNNQLIAGGLHAKVITKGEISV  
VPMRLDASLPVILVGGSGQSCSGGDEPTLTLEPVMIMELYLAKESKSTFYR  
RDMGLTSSFSBAAYGWFPLCTVPADQPVRLTQLPENGMNAPITDFFOCD"

## CDS

1..1282  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
73..540  
/note="unassigned protein product"  
/codon\_start=1  
/protein\_id="CAC27298.1"  
/db\_xref="GI:12579180"  
/translation="MVLGALCFPMKDSALKVLIHNNQLIAGGLHAKVITKGEISV  
VPMRLDASLPVILVGGSGQSCSGGDEPTLTLEPVMIMELYLAKESKSTFYR  
RDMGLTSSFSBAAYGWFPLCTVPADQPVRLTQLPENGMNAPITDFFOCD"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 1282;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGGACTCGGCAATGAAGTGCCTTTAT 60  
DB 73 ATGGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGGACTCGGCAATGAAGTGCCTTTAT 132  
QY 61 CTGCAATTAATACCAAGCTTCTAGCTGAGAGGCTGATGACAGGAAAGTCAATTAAGGTGAA 120  
DB 133 CTGCAATTAATACCAAGCTTCTAGCTGAGAGGCTGATGACAGGAAAGTCAATTAAGGTGAA 192  
QY 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGATGACAGCTGTCCCGTCACTCGGCT 180  
DB 193 GAGATCAGCGTGTGCTCCCAATCGGTGAGATGACAGCTGTCCCGTCACTCGGCT 252  
QY 181 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGTGGGGCAGAGCCGACTTAACACTA 240  
DB 253 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGTGGGGCAGAGCCGACTTAACACTA 312  
QY 241 GAGCAGTGAACATCATGAGCTTATCTTGTGTCCAGGAATCCAGAGCTTCACTTC 300  
DB 313 GAGCAGTGAACATCATGAGCTTATCTTGTGTCCAGGAATCCAGAGCTTCACTTC 372  
QY 301 TACCGGGGGGACATGGGGCTTCACTCGAGCTTCCAGTGGGTGCTTCCCGGCTGTTTC 360  
DB 373 TACCGGGGGGACATGGGGCTTCACTCGAGCTTCCAGTGGGTGCTTCCCGGCTGTTTC 432  
QY 361 CTGTGACGCGTGTCTGAGAGCCGATGACCTGTGACACTCACCCAGCTTCCGAGATGCT 420  
DB 433 CTGTGACGCGTGTCTGAGAGCCGATGACCTGTGACACTCACCCAGCTTCCGAGATGCT 492  
QY 421 GGCTGGAATGCCCATCAGACTTCTACTTCCAGAGGTGACTAG 468  
DB 493 GGCTGGAATGCCCATCAGACTTCTACTTCCAGAGGTGACTAG 540

## RESULT 12

AF201830 1288 bp mRNA linear PRI 16-JAN-2000  
LOCUS AF201830  
DEFINITION Homo sapiens FI11 delta mRNA, complete cds.  
ACCESSION AF201830  
VERSION AF201830.1 GI:6694387  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1288)  
AUTHORS Smith, D.E., Renshaw, B.R., Ketchum, R.R., Kudin, M., Garika, K.E. and  
TITLE Sime, J.B.  
JOURNAL Four new members expand the interleukin-1 superfamily  
PUBMED 10625660  
REFERENCE 2 (bases 1 to 1288)  
AUTHORS Sime, J.B.  
TITLE Direct Submission  
JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51  
University Street, Seattle, WA 98101, USA

FEATURES Location/Qualifiers  
source 1..1288  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/map="2q; between D2S121 and D2S110"  
28..495  
/note="Similar to IL-1"  
/codon\_start=1  
/product="FI11 delta"

## CDS

1..1288  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/map="2q; between D2S121 and D2S110"  
28..495  
/note="Similar to IL-1"  
/codon\_start=1  
/product="FI11 delta"

/protein\_id="AAF25210.1"  
 /db\_xref="GI:6694388"  
 /translation="MVLGALCFPMKDSALKVLYLHNNLLAGSLHAGKVIKREISV  
 VPRNMDASISPVILGVQSGSCISCVGEPTITLPRVIMETLYLAKSKSTFPR  
 RDMGLTSSPFSAMPGMFLCTVPEADPVLTLPPNGWNAPIITDFPQCD"

## ORIGIN

Query Match 100.0%; Score 468; DB 8; Length 1288;  
 Best Local Similarity 100.0%; Pred. No. 1,8e-107; Indels 0; Gaps 0;  
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAAGCTCTTAT 60  
 DB 28 ATGCTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAAGCTCTTAT 87  
 QY 61 CTGATATATACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGAA 120  
 DB 88 CTGATATATACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGAA 147  
 QY 121 GAGATCAGCGGTGTCCCAATCGGTGAGTGCAGACCTGTCCCGCTGATCGGGGT 180  
 DB 148 GAGATCAGCGGTGTCCCAATCGGTGAGTGCAGACCTGTCCCGCTGATCGGGGT 207  
 QY 181 GTCCAGGCTGAGAACCAAGTGCCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACACTA 240  
 DB 208 GTCCAGGCTGAGAACCAAGTGCCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACACTA 267  
 QY 241 GAGCAGTGAACATCATGAGAGCTCTATCTTGTGTCCAGAGAAATCCAGAGCTTCACTTC 300  
 DB 268 GAGCAGTGAACATCATGAGAGCTCTATCTTGTGTCCAGAGAAATCCAGAGCTTCACTTC 327  
 QY 301 TACCGGGGGGACATGGGGCTCACTCCAGCTTGAGTCCGCTGCTACCGGGGCTGGTTC 360  
 DB 328 TACCGGGGGGACATGGGGCTCACTCCAGCTTGAGTCCGCTGCTACCGGGGCTGGTTC 387  
 QY 361 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGACACTCAACCAAGCTTCCGAGAAATGCT 420  
 DB 388 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGACACTCAACCAAGCTTCCGAGAAATGCT 447  
 QY 421 GGTGGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 468  
 DB 448 GGTGGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 495

## RESULT 13

AX080389 2563 bp DNA linear PAT 22-FEB-2001  
 LOCUS AX080389 Sequence 1 from Patent WO0105974.  
 DEFINITION AX080389  
 ACCESSION AX080389  
 VERSION AX080389.1 GI:13159840  
 KEYWORDS

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 Homiidae; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

AUTHORS Nicklin, M. and Barton, I.  
 TITLE The 11-11 gene and polypeptide products  
 JOURNAL Patent: WO 0105974-A 1 25-JAN-2001

FEATURES location/Qualifiers  
 source 1..2563  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2563;  
 Best Local Similarity 100.0%; Pred. No. 1,8e-107; Indels 0; Gaps 0;  
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGCTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAAGCTCTTAT 60

DB 30 ATGCTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAAGCTCTTAT 89  
 QY 61 CTGATATATACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGAA 120  
 DB 90 CTGATATATACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGAA 149  
 QY 121 GAGATCAGCGGTGTCCCAATCGGTGAGTGCAGACCTGTCCCGCTGATCGGGGT 180  
 DB 150 GAGATCAGCGGTGTCCCAATCGGTGAGTGCAGACCTGTCCCGCTGATCGGGGT 209  
 QY 181 GTCCAGGCTGAGAACCAAGTGCCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACACTA 240  
 DB 210 GTCCAGGCTGAGAACCAAGTGCCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACACTA 269  
 QY 241 GAGCAGTGAACATCATGAGAGCTCTATCTTGTGTCCAGAGAAATCCAGAGCTTCACTTC 300  
 DB 270 GAGCAGTGAACATCATGAGAGCTCTATCTTGTGTCCAGAGAAATCCAGAGCTTCACTTC 329  
 QY 301 TACCGGGGGGACATGGGGCTCACTCCAGCTTGAGTCCGCTGCTACCGGGGCTGGTTC 360  
 DB 330 TACCGGGGGGACATGGGGCTCACTCCAGCTTGAGTCCGCTGCTACCGGGGCTGGTTC 389  
 QY 361 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGACACTCAACCAAGCTTCCGAGAAATGCT 420  
 DB 390 CTGTGACAGGTGCTGGAAGCCGATCAGCTGTGACACTCAACCAAGCTTCCGAGAAATGCT 449  
 QY 421 GGTGGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 468  
 DB 450 GGTGGAATGCCCCCATCAGACTTCTACTTCCAGAGTGTACTAG 497

## RESULT 14

AX092420 2598 bp DNA linear PAT 21-MAR-2001  
 LOCUS AX092420 Sequence 151 from Patent WO0116318.  
 DEFINITION AX092420  
 ACCESSION AX092420  
 VERSION AX092420.1 GI:13444524  
 KEYWORDS

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 Homiidae; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

AUTHORS Baton, D.L., Pilvaroff, E., Gerritsen, M.E., Goddard, A.,  
 Goddard, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and  
 Wood, W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same

JOURNAL Patent: WO 0116318-A 151 08-MAR-2001;  
 Genentech, Inc. (US)

FEATURES location/Qualifiers  
 source 1..2598  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2598;  
 Best Local Similarity 100.0%; Pred. No. 1,8e-107; Indels 0; Gaps 0;  
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGCTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAAGCTCTTAT 60  
 DB 67 ATGCTCTGAGTGGGGCGCTGTGCTTCGAAATGAAGACTCGGCAATGAAAGCTCTTAT 126  
 QY 61 CTGATATATACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGAA 120  
 DB 127 CTGATATATACCAAGCTTCTAGCTGAGAGGCTGCATGAGGAAAGTCAATTAAGTGAA 186  
 QY 121 GAGATCAGCGGTGTCCCAATCGGTGAGTGCAGACCTGTCCCGCTGATCGGGGT 180

Db 187 GAGATCAGCGTGGTCCCAATCGGTGGATGATGACGAGCTGTCCCTCATCTGGGT 246  
Qy 181 GTCCAGGGTGGAAAGCCAGTGTCTCATGTGGGGTGGGGGCAAGAGCCGACTTAAACCTA 240  
Db 247 GTCCAGGGTGGAAAGCCAGTGTCTCATGTGGGGTGGGGGCAAGAGCCGACTTAAACCTA 306  
Qy 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCCAGAGCTTCACTTC 300  
Db 307 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCCAGAGCTTCACTTC 366  
Qy 301 TACCGGCGGGAACATGAGGCTCTACCTCCAGCTTGTGAGTCCGCTGCTTACCCGGCTGTTT 360  
Db 367 TACCGGCGGGAACATGAGGCTCTACCTCCAGCTTGTGAGTCCGCTGCTTACCCGGCTGTTT 426  
Qy 361 CTGTGACAGGTGCTGTAAGCCGATTCAGCTTGTCAAGTCCAGCTTCCCGAAGATGTT 420  
Db 427 CTGTGACAGGTGCTGTAAGCCGATTCAGCTTGTCAAGTCCAGCTTCCCGAAGATGTT 486  
Qy 421 GGCTGGAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAG 468  
Db 487 GGCTGGAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAG 534

RESULT 15  
AX454730 2598 bp DNA linear PAT 06-JUL-2002  
LOCUS AX454730 Sequence 315 from Patent WO0208284.  
DEFINITION AX454730  
ACCESSION AX454730 GI:21713989  
VERSION AX454730.1  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Gadowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.

## TITLE

Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

## JOURNAL

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Gadowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

## FEATURES

## source

1..2598 location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2598;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTCTGAGTGGGGGCGCTGTGCTCCGATGGAAGAGCTGGCATTTAAAGTCTTAT 60  
Db 67 ATGGCTCTGAGTGGGGGCGCTGTGCTCCGATGGAAGAGCTGGCATTTAAAGTCTTAT 126  
Qy 61 CTGCATATAAACAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAAGTCAATTAAGTGA 120  
Db 127 CTGCATATAAACAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAAGTCAATTAAGTGA 186  
Qy 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCAAGCTGTCCCGCTCATCTGGGT 180  
Db 187 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCAAGCTGTCCCGCTCATCTGGGT 246

Qy 181 GTCCAGGGTGGAAAGCCAGTGTCTCATGTGGGGTGGGGGCAAGAGCCGACTTAAACCTA 240  
Db 247 GTCCAGGGTGGAAAGCCAGTGTCTCATGTGGGGTGGGGGCAAGAGCCGACTTAAACCTA 306  
Qy 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCCAGAGCTTCACTTC 300  
Db 307 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCCAGAGCTTCACTTC 366  
Qy 301 TACCGGCGGGAACATGAGGCTCTACCTCCAGCTTGTGAGTCCGCTGCTTACCCGGCTGTTT 360  
Db 367 TACCGGCGGGAACATGAGGCTCTACCTCCAGCTTGTGAGTCCGCTGCTTACCCGGCTGTTT 426  
Qy 361 CTGTGACAGGTGCTGTAAGCCGATTCAGCTTGTCAAGTCCAGCTTCCCGAAGATGTT 420  
Db 427 CTGTGACAGGTGCTGTAAGCCGATTCAGCTTGTCAAGTCCAGCTTCCCGAAGATGTT 486  
Qy 421 GGCTGGAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAG 468  
Db 487 GGCTGGAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAG 534

RESULT 16  
AX491208 2598 bp DNA linear PAT 16-AUG-2002  
LOCUS AX491208 Sequence 315 from Patent WO020690.  
DEFINITION AX491208  
ACCESSION AX491208 GI:22323941  
VERSION AX491208.1  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Gadowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.

## TITLE

Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

## JOURNAL

Genentech, Inc. (US)  
Patent: WO 020690-A 315 03-JAN-2002;

## FEATURES

## source

1..2598 location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2598;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTCTGAGTGGGGGCGCTGTGCTCCGATGGAAGAGCTGGCATTTAAAGTCTTAT 60  
Db 67 ATGGCTCTGAGTGGGGGCGCTGTGCTCCGATGGAAGAGCTGGCATTTAAAGTCTTAT 126  
Qy 61 CTGCATATAAACAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAAGTCAATTAAGTGA 120  
Db 127 CTGCATATAAACAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAAGTCAATTAAGTGA 186  
Qy 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCAAGCTGTCCCGCTCATCTGGGT 180  
Db 187 GAGATCAGCGTGTGCTCCCAATCGGTGCTGATGCAAGCTGTCCCGCTCATCTGGGT 246  
Qy 181 GTCCAGGGTGGAAAGCCAGTGTCTCATGTGGGGTGGGGGCAAGAGCCGACTTAAACCTA 240  
Db 247 GTCCAGGGTGGAAAGCCAGTGTCTCATGTGGGGTGGGGGCAAGAGCCGACTTAAACCTA 306  
Qy 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCCAGAGCTTCACTTC 300  
Db 307 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCCAGAGCTTCACTTC 366

QY 301 TACCGGCGGACATGAGGCTCAGCTCCAGCTTCAGTGGCTGCTACCCGGCTGGTTC 360  
DB 367 TACCGGCGGACATGAGGCTCAGCTCCAGCTTCAGTGGCTGCTACCCGGCTGGTTC 426  
QY 361 CTGTGACAGGCTGCTGAGAGCCGATCAGCTTCAGACTCACCAGCTTCCGAGAAATGT 420  
DB 427 CTGTGACAGGCTGCTGAGAGCCGATCAGCTTCAGACTCACCAGCTTCCGAGAAATGT 486  
QY 421 GCGTGAATGCCCCATCAGACTTCTACTTCCAGCAGTGTGACTAG 468  
DB 487 GCGTGAATGCCCCATCAGACTTCTACTTCCAGCAGTGTGACTAG 534

RESULT 17  
AY359117

LOCUS AY359117 2598 bp mRNA linear PRI 03-OCT-2003  
DEFINITION Homo sapiens clone DNA96787 IL1H1 (UNQ1896) mRNA, complete cds.  
ACCESSION AY359117.1 GI:37183350  
VERSION AY359117.1  
KEYWORDS FLI CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 2598)  
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,  
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,  
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,  
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,  
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,  
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,  
Stinson, J., Vagstad, A., Vandlen, R., Watanabe, C., Wileand, D., Woods, K.,  
Xie, M.H., Yamaoka, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,  
Goddard, A., Wood, W.I. and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 2598)  
AUTHORS Clark, H.F.  
TITLE Direct Submission  
JOURNAL Submitted (01-ANG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
FEATURES  
source  
1. .2598  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DNA96787"  
1. .2598  
/locus\_tag="UNQ1896"  
67. .534  
/locus\_tag="UNQ1896"  
/note="PRO4342"  
/codon\_start=1  
/product="IL1H1"  
/protein\_id="AA089475.1"  
/db\_xref="GI:37183351"  
/translation="MVLGALCFPMKDSALKLVLYHNOLLGGLHAGKYLKGEISV  
VPRNKLASPLVITGLVGGSCICSGVGEPTLTLPVNMELYLAKSKSKTFPR  
RDMGLTSSFESAIYFQWFLCTVPEADQPVRLTQLPENGKNAFPTIDYFPOCD"

ORIGIN  
Query Match 100.0%; Score 468; DB 8; Length 2598;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTCTGAGTGGGCGCTGTGCTTCGGAATGAAGACTGGCAATGAAGGCTTTAT 60  
DB 67 ATGGTCTGAGTGGGCGCTGTGCTTCGGAATGAAGACTGGCAATGAAGGCTTTAT 126

QY 61 CTGCATATAACAGCTTCTAGCTGAGAGGCTGCATGACGAGGAAGTCAATTAAGGTGA 120  
DB 127 CTGCATATAACAGCTTCTAGCTGAGAGGCTGCATGACGAGGAAGTCAATTAAGGTGA 186  
QY 121 GAGATCAGCGTGTGCTCCCAATGCGTGTGATCCAGCTGTCCCTCATCTGGGT 180  
DB 187 GAGATCAGCGTGTGCTCCCAATGCGTGTGATCCAGCTGTCCCTCATCTGGGT 246  
QY 181 GTCCAGGTTGAACCAAGCTGCTGTCATGTGGGGTGGGAGCCGACCTTAACATA 240  
DB 247 GTCCAGGTTGAACCAAGCTGCTGTCATGTGGGGTGGGAGCCGACCTTAACATA 306  
QY 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGATGTCGAAGATCAAGAGCTTCACTTC 300  
DB 307 GAGCCAGTGAACATCATGAGAGCTTATCTTGATGTCGAAGATCAAGAGCTTCACTTC 366  
QY 301 TACCGGCGGACATGAGGCTCAGCTTCCAGCTTCAGTGGCTGCTTACCCGGCTGGTTC 360  
DB 367 TACCGGCGGACATGAGGCTCAGCTTCCAGCTTCAGTGGCTGCTTACCCGGCTGGTTC 426  
QY 361 CTGTGACAGGCTGCTGAGAGCCGATCAGCTTCAGACTCACCAGCTTCCGAGAAATGT 420  
DB 427 CTGTGACAGGCTGCTGAGAGCCGATCAGCTTCAGACTCACCAGCTTCCGAGAAATGT 486  
QY 421 GCGTGAATGCCCCATCAGACTTCTACTTCCAGCAGTGTGACTAG 468  
DB 487 GCGTGAATGCCCCATCAGACTTCTACTTCCAGCAGTGTGACTAG 534

RESULT 18  
HSA242738

LOCUS HSA242738 2604 bp mRNA linear PRI 15-APR-2005  
DEFINITION Homo sapiens mRNA for interleukin-1-like protein 1 (IL1L1 gene)  
transcript 2.  
ACCESSION AJ242738  
VERSION AJ242738.1 GI:6165335  
KEYWORDS IL1L1 gene; interleukin-1-like protein 1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1  
Barton, J.L., Herbst, R., Bosio, D., Higgins, L., and Nicklin, M.J.  
A tissue specific IL-1 receptor antagonist homolog from the IL-1  
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities  
Eur. J. Immunol. 30 (11), 3299-3308 (2000)  
JOURNAL 11093146  
PUBMED 11093146  
REFERENCE 2 (bases 1 to 2604)  
AUTHORS Nicklin, M.J.  
TITLE Direct Submission  
JOURNAL Submitted (09-JUN-1992) Nicklin M.J., Division of Molecular and  
Genetic Medicine, University of Sheffield, Royal Hallamshire  
Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM  
FEATURES  
source  
1. .2604  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/map="2q12-13"  
/tissue\_type="placenta"  
/note="Between IL1B and IL1RN"  
1. .2604  
/gene="IL1L1"  
/name="IL1L1"  
73. .540  
/function="putative cytokine"  
/codon\_start=1  
/product="interleukin-1-like protein 1"  
/protein\_id="CAB59823.1"  
/db\_xref="GI:6165336"  
/db\_xref="G0A:Q9UBH0"

```

/db_xref="InterPro:IPR000975"
/db_xref="InterPro:IPR003296"
/db_xref="InterPro:IPR003297"
/db_xref="InterPro:IPR008996"
/db_xref="UniProt/Swiss-Prot:Q9UBH0"
/translation="MVLGALCFRMDKSLKVLVYLNHNNLLAGLHAKYIKGEISV
VPRMLDASLPVILGVGSGSGLCPVIMELTYGAKSKSFTFYR
RDMGLTSSFESNAIPGMFLCTVPEADQPVRLTLPENGMNAITDPYQQCD"
2604
/gene="IL1L1"

```

```

Query Match      100.0%; Score 468; DB 8; Length 2604;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAGAGACTCGGATTGAAGTGTCTTAT 60
DB 73 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAGAGACTCGGATTGAAGTGTCTTAT 132
QY 61 CTGCATTAATTAACCAAGCTTTCTAGCTGAGAGGCTGATGCAAGAGAGTCAATTAAGTGAA 120
DB 133 CTGCATTAATTAACCAAGCTTTCTAGCTGAGAGGCTGATGCAAGAGAGTCAATTAAGTGAA 192
QY 121 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTGTCCCGCTCATCTGGGT 180
DB 193 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTGTCCCGCTCATCTGGGT 252
QY 181 GTCCAGGGTGAAGACAGTGTGCTGATGAGGGTGGGGAGAGCCGACTTAACACTA 240
DB 253 GTCCAGGGTGAAGACAGTGTGCTGATGAGGGTGGGGAGAGCCGACTTAACACTA 312
QY 241 GAGCGATGAACATCATGAGAGCTTATCTGTGTGCCAAGAAATCCAGAGCTTCACTTC 300
DB 313 GAGCGATGAACATCATGAGAGCTTATCTGTGTGCCAAGAAATCCAGAGCTTCACTTC 372
QY 301 TACCGGGGGAGACATGAGGCTCCTCAGCTTCAGTGTGGGCTCTACCGGGCTGTTC 360
DB 373 TACCGGGGGAGACATGAGGCTCCTCAGCTTCAGTGTGGGCTCTACCGGGCTGTTC 432
QY 361 CTGTGACCGGTGCTGTGAAGCCGATGACCTGTGCTGACTCAACCGCTTCCGAGATGGT 420
DB 433 CTGTGACCGGTGCTGTGAAGCCGATGACCTGTGCTGACTCAACCGCTTCCGAGATGGT 492
QY 421 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGAGTGTACTAG 468
DB 493 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGAGTGTACTAG 540

```

RESULT 19  
HSA242737 2613 bp mRNA linear PRI 15-APR-2005  
LOCUS Homo sapiens mRNA for interleukin-1-like protein-1 (IL1L1 gene), transcribed 1.

ACCESSION AJ242737.1 GI:6165333  
VERSION AJ242737.1 GI:6165333  
KEYWORDS IL1L1 gene; interleukin-1-like protein-1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 Bartsch, J.L., Herbst, R., Bosio, D., Higgins, L. and Nicklin, M.J.  
A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities  
Eur. J. Immunol. 30 (11), 3299-3308 (2000)

REFERENCE 2 (bases 1 to 2613)  
AUTHORS Nicklin, M.J.  
TITLE Direct Submersion  
JOURNAL Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire

```

FEATURES
source Hospital, Glossop Road, Sheffield, S10 2UF, UNITED KINGDOM
location/Qualifiers
1..2613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="2"
/map="2q12-13"
/risue_type="placenta"
/note="Between IL1B and IL1RN"
1..2613
/gene="IL1L1"
82..549
/gene="IL1L1"
/function="putative cytokine"
/codon_start=1
/product="interleukin-1-like protein-1"
/protein_id="CAB59822.1"
/db_xref="GI:6165334"
/db_xref="GOA:Q9UBH0"
/db_xref="InterPro:IPR000975"
/db_xref="InterPro:IPR003296"
/db_xref="InterPro:IPR003297"
/db_xref="InterPro:IPR008996"
/db_xref="UniProt/Swiss-Prot:Q9UBH0"
/translation="MVLGALCFRMDKSLKVLVYLNHNNLLAGLHAKYIKGEISV
VPRMLDASLPVILGVGSGSGLCPVIMELTYGAKSKSFTFYR
RDMGLTSSFESNAIPGMFLCTVPEADQPVRLTLPENGMNAITDPYQQCD"
2613
/gene="IL1L1"
/citation={1}
/evidence=experimental

```

```

Query Match      100.0%; Score 468; DB 8; Length 2613;
Best Local Similarity 100.0%; Pred. No. 1.8e-107;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAGAGACTCGGATTGAAGTGTCTTAT 60
DB 82 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAGAGACTCGGATTGAAGTGTCTTAT 141
QY 61 CTGCATTAATTAACCAAGCTTTCTAGCTGAGAGGCTGATGCAAGAGAGTCAATTAAGTGAA 120
DB 142 CTGCATTAATTAACCAAGCTTTCTAGCTGAGAGGCTGATGCAAGAGAGTCAATTAAGTGAA 201
QY 121 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTGTCCCGCTCATCTGGGT 180
DB 202 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTGTCCCGCTCATCTGGGT 261
QY 181 GTCCAGGGTGAAGACAGTGTGCTGATGAGGGTGGGGAGAGCCGACTTAACACTA 240
DB 262 GTCCAGGGTGAAGACAGTGTGCTGATGAGGGTGGGGAGAGCCGACTTAACACTA 321
QY 241 GAGCGATGAACATCATGAGAGCTTATCTGTGTGCCAAGAAATCCAGAGCTTCACTTC 300
DB 322 GAGCGATGAACATCATGAGAGCTTATCTGTGTGCCAAGAAATCCAGAGCTTCACTTC 381
QY 301 TACCGGGGGAGACATGAGGCTCCTCAGCTTGAAGTGTGCTGCTTACCGGGCTGTTC 360
DB 382 TACCGGGGGAGACATGAGGCTCCTCAGCTTGAAGTGTGCTGCTTACCGGGCTGTTC 441
QY 361 CTGTGACCGGTGCTGTGAAGCCGATGACCTGTGCTGACTCAACCGCTTCCGAGATGGT 420
DB 442 CTGTGACCGGTGCTGTGAAGCCGATGACCTGTGCTGACTCAACCGCTTCCGAGATGGT 501
QY 421 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGAGTGTACTAG 468
DB 502 GCGTGAATGCCCCCATCAGACTTCTACTTCCAGAGAGTGTACTAG 549

```

RESULT 20  
BD211435

LOCUS BD211435 2648 bp DNA linear PAT 17-JUL-2003  
 DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.  
 ACCESSION BD211435  
 VERSION BD211435.1 GI:33021205  
 KEYWORDS JP 2002510492-A/4.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 2648)  
 REFERENCE 1 (bases 1 to 2648)  
 AUTHORS Ford J. and Pace A.  
 TITLE A novel interleukin-1 receptor antagonist and uses thereof  
 JOURNAL Patent: JP 2002510492-A 4 09-APR-2002;  
 HYSEO INC  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002510492-A/4  
 PD 09-APR-2002  
 PR 05-APR-1999 JP 2000542457  
 PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR  
 20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR  
 31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR  
 11-FEB-1999 US 09/251370  
 PI JOHN FORD, ANN PACE  
 PC C12N15/09, A61K38/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15,  
 PC C12N1/19,  
 PC C12N1/21, C12N5/10, C12Q1/68, G01N33/50, G01N33/566, G01N33/68, PC  
 C12N15/00,  
 PC A61K37/02, C12N5/00  
 CC A novel interleukin-1 receptor antagonist and uses thereof FH  
 Key Location/Qualifiers  
 FT source 1..2648  
 FT Location/Qualifiers  
 1..2648  
 /organism="Homo sapiens (human)"  
 /molecule="genomic DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 100.0%; Score 468; DB 6; Length 2648;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGGATGAAGTCTTTAT 60  
 Db 62 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGGATGAAGTCTTTAT 121  
 Oy 61 CTGCATATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGGAAGTCAATTAAGTGAA 120  
 Db 122 CTGCATATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGGAAGTCAATTAAGTGAA 181  
 Oy 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGGATCCAGCTGTCCCGCTCATCTGGGT 180  
 Db 182 GAGATCAGCGTGTGCTCCCAATCGGTGCTGGATCCAGCTGTCCCGCTCATCTGGGT 241  
 Oy 181 GTCCAGAGTGAAGCCAGTCTGTCTCATGTGGGGTGGGGGAGAGCCGACTTAACTA 240  
 Db 242 GTCCAGAGTGAAGCCAGTCTGTCTCATGTGGGGTGGGGGAGAGCCGACTTAACTA 301  
 Oy 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCGAAGGATCCAGAGCTTCACTTC 300  
 Db 302 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCGAAGGATCCAGAGCTTCACTTC 361  
 Oy 301 TACCGGCGGAGCATGGGGCTTACCTTCAGCTTCGAGTCGGCTGCTTACCGGGCTGTTTC 360  
 Db 362 TACCGGCGGAGCATGGGGCTTACCTTCAGCTTCGAGTCGGCTGCTTACCGGGCTGTTTC 421  
 Oy 361 CTGTGACGCGTGTCTGAAGCCGATCAGCTGTGAGATCACCAGCTTCCCGAAGATG 420  
 Db 422 CTGTGACGCGTGTCTGAAGCCGATCAGCTGTGAGATCACCAGCTTCCCGAAGATG 481  
 Oy 421 GGCTGAATGCCCCCATCAGAGCTTCTACTTCAGAGTGTGACTAG 468

Db 482 GGCTGAATGCCCCCATCAGAGCTTCTACTTCCAGAGTGTGACTAG 529  
 RESULT 21  
 LOCUS AR181995 2648 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 6 from patent US 6337072.  
 ACCESSION AR181995  
 VERSION AR181995.1 GI:20224911  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2648)  
 AUTHORS Ford J. and Pace A.  
 TITLE Interleukin-1 receptor antagonist and recombinant production thereof  
 JOURNAL Patent: US 6337072-A 6 08-JAN-2002;  
 FEATURES location/Qualifiers  
 source 1..2648  
 /organism="unknown"  
 /molecule="unassigned DNA"  
 ORIGIN  
 Query Match 100.0%; Score 468; DB 6; Length 2648;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGGATGAAGTCTTTAT 60  
 Db 62 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGAGCTCGGATGAAGTCTTTAT 121  
 Oy 61 CTGCATATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGGAAGTCAATTAAGTGAA 120  
 Db 122 CTGCATATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGGAAGTCAATTAAGTGAA 181  
 Oy 121 GAGATCAGCGTGTGCTCCCAATCGGTGCTGGATCCAGCTGTCCCGCTCATCTGGGT 180  
 Db 182 GAGATCAGCGTGTGCTCCCAATCGGTGCTGGATCCAGCTGTCCCGCTCATCTGGGT 241  
 Oy 181 GTCCAGAGTGAAGCCAGTCTGTCTCATGTGGGGTGGGGGAGAGCCGACTTAACTA 240  
 Db 242 GTCCAGAGTGAAGCCAGTCTGTCTCATGTGGGGTGGGGGAGAGCCGACTTAACTA 301  
 Oy 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCGAAGGATCCAGAGCTTCACTTC 300  
 Db 302 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCGAAGGATCCAGAGCTTCACTTC 361  
 Oy 301 TACCGGCGGAGCATGGGGCTTACCTTCAGCTTCGAGTCGGCTGCTTACCGGGCTGTTTC 360  
 Db 362 TACCGGCGGAGCATGGGGCTTACCTTCAGCTTCGAGTCGGCTGCTTACCGGGCTGTTTC 421  
 Oy 361 CTGTGACGCGTGTCTGAAGCCGATCAGCTGTGAGATCACCAGCTTCCCGAAGATG 420  
 Db 422 CTGTGACGCGTGTCTGAAGCCGATCAGCTGTGAGATCACCAGCTTCCCGAAGATG 481  
 Oy 421 GGCTGAATGCCCCCATCAGAGCTTCTACTTCCAGAGTGTGACTAG 468  
 Db 482 GGCTGAATGCCCCCATCAGAGCTTCTACTTCCAGAGTGTGACTAG 529  
 RESULT 22  
 LOCUS AR221129 2648 bp DNA linear PAT 26-SEP-2002  
 DEFINITION Sequence 6 from patent US 6426191.  
 ACCESSION AR221129  
 VERSION AR221129.1 GI:23328014  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2648)  
 Unclassified.

AUTHORS Ford, J. and Pace, A.  
TITLE Assays involving an IL-1 receptor antagonist  
JOURNAL Patent: US 6426191-A 6 30-JUN-2002;  
HySeq, Inc.; Sunnyvale, CA

FEATURES  
SOURCE 1..2648  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2648;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGGATGAAGTCTTAT 60  
DB 62 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGGATGAAGTCTTAT 121  
QY 61 CTGCATTAATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGAAAGTCATTAAAGTGAA 120  
DB 122 CTGCATTAATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGAAAGTCATTAAAGTGAA 181  
QY 121 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 180  
DB 182 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 241  
QY 181 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGGTGGGGAGGAGCCGACTTAACACTA 240  
DB 242 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGGTGGGGAGGAGCCGACTTAACACTA 301  
QY 241 GAGCAGTGAACATCATGAGCTTATCTTGATGCCAAGATCCAAAGCTTCAACCTTC 300  
DB 302 GAGCAGTGAACATCATGAGCTTATCTTGATGCCAAGATCCAAAGCTTCAACCTTC 361  
QY 301 TACCGGCGGAGCATGAGGCTTCACTTCAAGTGTGCTGCTTACCGGCTGCTTC 360  
DB 362 TACCGGCGGAGCATGAGGCTTCACTTCAAGTGTGCTGCTTACCGGCTGCTTC 421  
QY 361 CTGTGACGCGTGTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 420  
DB 422 CTGTGACGCGTGTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 481  
QY 421 GGCTGGAATGCCCCATCAAGACTTCTACTTCCAGCAGTGTGACTAG 468  
DB 482 GGCTGGAATGCCCCATCAAGACTTCTACTTCCAGCAGTGTGACTAG 529

## RESULT 23

AR302957 2648 bp DNA linear PAT 12-JUN-2003  
LOCUS AR302957  
DEFINITION Sequence 6 from patent US 6541623.  
ACCESSION AR302957  
VERSION AR302957.1 GI:31691557  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2648)  
AUTHORS Ford, J., Ho, A.S.-Y. and Pace, A.  
TITLE Interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: US 6541623-A 6 01-APR-2003;  
HySeq, Inc.; Sunnyvale, CA

FEATURES  
SOURCE 1..2648  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2648;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGGATGAAGTCTTAT 60

DB 62 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGGATGAAGTCTTAT 121  
QY 61 CTGCATTAATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGAAAGTCATTAAAGTGAA 120  
DB 122 CTGCATTAATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGAAAGTCATTAAAGTGAA 181  
QY 121 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 180  
DB 182 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 241  
QY 181 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGGTGGGGAGGAGCCGACTTAACACTA 240  
DB 242 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGGTGGGGAGGAGCCGACTTAACACTA 301  
QY 241 GAGCAGTGAACATCATGAGCTTATCTTGATGCCAAGATCCAAAGCTTCAACCTTC 300  
DB 302 GAGCAGTGAACATCATGAGCTTATCTTGATGCCAAGATCCAAAGCTTCAACCTTC 361  
QY 301 TACCGGCGGAGCATGAGGCTTCACTTCAAGTGTGCTGCTTACCGGCTGCTTC 360  
DB 362 TACCGGCGGAGCATGAGGCTTCACTTCAAGTGTGCTGCTTACCGGCTGCTTC 421  
QY 361 CTGTGACGCGTGTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 420  
DB 422 CTGTGACGCGTGTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 481  
QY 421 GGCTGGAATGCCCCATCAAGACTTCTACTTCCAGCAGTGTGACTAG 468  
DB 482 GGCTGGAATGCCCCATCAAGACTTCTACTTCCAGCAGTGTGACTAG 529

## RESULT 24

AX069309 2648 bp DNA linear PAT 25-JAN-2001  
LOCUS AX069309  
DEFINITION Sequence 6 from Patent WO0102571.  
ACCESSION AX069309  
VERSION AX069309.1 GI:12579181  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2648)  
AUTHORS Ford, J. and Pace, A.  
TITLE A interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: WO 0102571-A 6 11-JAN-2001;  
HYSEQ, INC. (US)

FEATURES  
SOURCE 1..2648  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 468; DB 6; Length 2648;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGGATGAAGTCTTAT 60  
DB 62 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGGATGAAGTCTTAT 121  
QY 61 CTGCATTAATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGAAAGTCATTAAAGTGAA 120  
DB 122 CTGCATTAATAACCAAGCTTTAGCTGAGAGGCTGCATCAGGAAAGTCATTAAAGTGAA 181  
QY 121 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 180  
DB 182 GAGATCAGCGTGTGCTGCAATCGGTGCTGATGCAAGCTTCTCCCTGATCTGGGT 241  
QY 181 GTCCAGGCTGGAAGCCAGTGTCTGATGAGGGGTGGGGAGGAGCCGACTTAACACTA 240



Db 242 GTCCAGGGGTGAGACAGAGTGCCTGTCATGTGGGGGGGAGAGCCAGCCTCTAACACTA 301  
 Oy 241 GAGCAGTGAACATCATGAGAGCTCTATTTGGTGCAGAGATCCAAAGCTTCACTTC 300  
 Db 302 GAGCAGTGAACATCATGAGAGCTCTATTTGGTGCAGAGATCCAAAGCTTCACTTC 361  
 Oy 301 TACCGGCGGAGCATGAGGAGCTCACTCCAGCTTCCAGTGGGCTTACCGGGGCTGTTG 360  
 Db 362 TACCGGCGGAGCATGAGGAGCTCACTCCAGCTTCCAGTGGGCTTACCGGGGCTGTTG 421  
 Oy 361 CTGTGACAGGCTGCTGAGAGCCGATCAGCTGTGACAGTCAACCCAGCTTCCGAGATGAT 420  
 Db 422 CTGTGACAGGCTGCTGAGAGCCGATCAGCTGTGACAGTCAACCCAGCTTCCGAGATGAT 481  
 Oy 421 GGCTGGAATGCCCTCATCAGACTTCTTACTTCCAGCAGTGTGACTAG 468  
 Db 482 GGCTGGAATGCCCTCATCAGACTTCTTACTTCCAGCAGTGTGACTAG 529

RESULT 25  
 LOCUS BC024747 2692 bp mRNA linear PRI 30-JUN-2004  
 DEFINITION Homo sapiens interleukin 1 family, member 5 (delta), transcript variant 2, mRNA (cdna clone MGC:29840 IMAGE:4996939), complete cds.  
 ACCESSION BC024747  
 VERSION BC024747.1 GI:19353229  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo  
 1 (bases 1 to 2692)  
 Strauberg, R.L., Felngold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hele, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Cabavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wolley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vialalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fehey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmeitz, J., Myers, R.M., Butcherfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E., Schmeitz, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 2 (bases 1 to 2692)  
 Strauberg, R.  
 Direct Submission  
 Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC) Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabp@remail.nih.gov](mailto:cgabp@remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)  
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louie, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: <http://image.llnl.gov>  
 Series: IRAX Plate: 42 Row: K Column: 16  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894309.

## FEATURES

## source

1..2692

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="MGC:29840 IMAGE:4996939"

/tissue\_type="Placenta, choriocarcinoma"

/clone\_id="NIH\_MGC\_10"

/lab\_host="DH10B"

/note="Vector: pCMV-SPORT6"

## gene

1..2692

/gene="IL1F5"

/note="synonyms: FIIL1 (DELTA), FIIL2, IL1RP3, IL1H1, FIIL1, IL1L1, MGC29840"

/db\_xref="GeneID:26525"

/db\_xref="MIM:605507"

134..601

/gene="IL1F5"

/codon\_start=1

/product="interleukin 1 family, member 5"

/protein\_id="AAH24747.1"

/db\_xref="GI:19353230"

/db\_xref="GeneID:26525"

/db\_xref="MIM:605507"

/translation="MVISGALCFERKDSALKVLYLNHNNQLAGIHAQKIVKEISIVPKNMIDASLSPVILGVQGSOCISCVQEPITLTPVIMELYLAKESKSTFPR

RDMLTSSPSSAAYPGWFLCTVPRADQVRLTQLENGWMAPIITDFVFOCD"

## CDS

## ORIGIN

## Query Match

100.0%; Score 468; DB 8; Length 2692;

Best Local Similarity 100.0%; Pred. No. 1.8e-107;

Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCTGAGTGGGGGCTGTGCTCCGATGAAGAGCTGGATTGAAGGCTTAT 60  
 134 ATGGCTGAGTGGGGGCTGTGCTCCGATGAAGAGCTGGATTGAAGGCTTAT 193  
 61 CTGCATATAACACAGCTTCTAGCTGAGAGGCTGCATGCAGAGGAGTCAATTAAGTGA 120  
 194 CTGCATATAACACAGCTTCTAGCTGAGAGGCTGCATGCAGAGGAGTCAATTAAGTGA 253  
 121 GAGATCAGCTGTGCTCCCAATCGGTGCTGATCCAGCTGTCCCGCTCATCTGGGT 180  
 254 GAGATCAGCTGTGCTCCCAATCGGTGCTGATCCAGCTGTCCCGCTCATCTGGGT 313  
 181 GTCCAGGTGAAGCCAGTGCCTGTCATGTGGGGTGGGGGAGCCGACCTTAACCTA 240  
 314 GTCCAGGTGAAGCCAGTGCCTGTCATGTGGGGTGGGGGAGCCGACCTTAACCTA 373  
 241 GAGCAGTGAACATCATGAGAGCTCTATTTGGTGCAGAGATCCAAAGCTTCACTTC 300  
 374 GAGCAGTGAACATCATGAGAGCTCTATTTGGTGCAGAGATCCAAAGCTTCACTTC 433  
 301 TACCGGCGGAGCATGAGGAGCTCACTCCAGCTTCCAGTGGGCTTACCGGGGCTGTTG 360  
 434 TACCGGCGGAGCATGAGGAGCTCACTCCAGCTTCCAGTGGGCTTACCGGGGCTGTTG 493  
 361 CTGTGACAGGCTGCTGAGAGCCGATCAGCTGTGACAGTCAACCCAGCTTCCGAGATGAT 420  
 494 CTGTGACAGGCTGCTGAGAGCCGATCAGCTGTGACAGTCAACCCAGCTTCCGAGATGAT 553  
 421 GGCTGGAATGCCCTCATCAGACTTCTTACTTCCAGCAGTGTGACTAG 468

Db 554 GGCTGGAATGCCCATCACAGACTTCTACTTCCAGCAGTGTACTAG 601

RESULT 26  
AF186094 2720 bp mRNA linear PRI 16-OCT-1999  
LOCUS Homo sapiens interleukin-1 receptor antagonist homolog (IL1HY1)  
DEFINITION mRNA, complete cds.  
ACCESSION AF186094  
VERSION AF186094.1 GI:6049804  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 2720)  
AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Dmanac,R. and Ford,J.E.  
TITLE IL1HY1: A novel interleukin-1 receptor antagonist gene  
JOURNAL Biochem. Biophys. Res. Commun. 263 (3), 702-706 (1999)  
PUBMED 10512743  
REFERENCE 2 (bases 1 to 2720)  
AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Dmanac,R. and Ford,J.E.  
TITLE Direct Submission  
JOURNAL Submitted (13-SEP-1999) Functional Genomics, HYSBO Inc., 670 Alhambra Ave., Sunnyvale, CA 94086, USA  
FEATURES  
source  
Location/Qualifiers  
1..2720  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
1..2720  
/gene="IL1HY1"  
163..630  
/gene="IL1HY1"  
/note="IL-1ra homolog"  
/codon\_start=1  
/product="interleukin-1 receptor antagonist homolog"  
/protein\_id="AA02757.1"  
/db\_xref="GI:6049805"  
/translation="MVLGALCFPMKDSALKVLYLHNNOLLAGLHAGKYIKGEISV VPRWLDLSPVILGVQSGOCLSCVGEPTLTLPVNMELYLAKSKSPTFYR RMDGLTSSFSAAYPGWFLCTVBPADQPVRLTQLPENGWNNAPITDVFQCDL"

ORIGIN  
Query Match 100.0%; Score 468; DB 8; Length 2720;  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCTCTGAGTGGGGGCTGTGCTCCGAAATGAAGACTGGCAATGAAGTGTCTTAT 60  
DB 163 ATGTCTCTGAGTGGGGGCTGTGCTCCGAAATGAAGACTGGCAATGAAGTGTCTTAT 222  
QY 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGATGACAGAGGAAGTCAATTAAGGTGA 120  
DB 223 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGATGACAGAGGAAGTCAATTAAGGTGA 282  
QY 121 GAGATCAAGCTGTCTCCCAATCGGTGCTGATGACCAAGCTGTCCCGGTCATCTGGGT 180  
DB 283 GAGATCAAGCTGTCTCCCAATCGGTGCTGATGACCAAGCTGTCCCGGTCATCTGGGT 342  
QY 181 GTCCAGAGGTGAAGCAAGCTGTCTGATGAGGGGTGGGGCGAGAGCCGACTTAACTA 240  
DB 343 GTCCAGAGGTGAAGCAAGCTGTCTGATGAGGGGTGGGGCGAGAGCCGACTTAACTA 402  
QY 241 GAGCAGAGCAATCATGAGACTCTATCTGTGGTCCAGAGATCCAAAGCTTCAACCTTC 300  
DB 403 GAGCAGAGCAATCATGAGACTCTATCTGTGGTCCAGAGATCCAAAGCTTCAACCTTC 462  
QY 301 TACCGCGCGGACATGAGGCTCACTCAGCTTCAGTGGGTGCTTACCGGGCTGTTC 360  
|||||

Db 463 TACCGCGCGGACATGAGGCTCACTCCAGCTTCAGTGGGTGCTTACCGGGCTGTTC 522

QY 361 CTGTGACAGGCTGCTGAGAGCGATTCAGCTGTGATCAATCCAGCTTCCGAGATGGT 420  
DB 523 CTGTGACAGGCTGCTGAGAGCGATTCAGCTGTGATCAATCCAGCTTCCGAGATGGT 582

QY 421 GGCTGGAATGCCCATCACAGACTTCTACTTCCAGCAGTGTACTAG 468  
DB 583 GGCTGGAATGCCCATCACAGACTTCTACTTCCAGCAGTGTACTAG 630

RESULT 27  
AY893100 468 bp mRNA linear SYN 29-MAR-2005  
LOCUS Synthetic construct Homo sapiens clone FLH141291.01L interleukin 1  
DEFINITION family member 5 (IL1F5) mRNA, partial cds.  
ACCESSION AY893100  
VERSION AY893100.1 GI:60810164  
KEYWORDS Human ORF Project.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 468)  
AUTHORS Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F., Shen,B., Hallack,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E., Williamson,J. and Labaer,J.  
TITLE Cloning of human full-length CDS in Creator (TM) recombinational vector system  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 468)  
AUTHORS Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F., Shen,B., Hallack,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E., Williamson,J. and Labaer,J.  
TITLE Direct Submission  
JOURNAL Submitted (05-JUN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA  
COMMENT This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the SalI and HindIII sites of the pNDR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.  
Location/Qualifiers  
1..468  
/organism="synthetic construct"  
/mol\_type="mRNA"  
/db\_xref="taxon:32630"  
/clone="FLH141291.01L"  
/lab\_host="Escherichia coli DH5alpha TI resistant"  
/note="derived from MGC template"  
1..>468  
/gene="IL1F5"  
1..>468  
/gene="IL1F5"  
/note="delta"  
/codon\_start=1  
/transl\_table=1  
/product="interleukin 1 family member 5"  
/protein\_id="AAK36138.1"  
/db\_xref="GI:60810165"  
/translation="MVLGALCFPMKDSALKVLYLHNNOLLAGLHAGKYIKGEISV VPRWLDLSPVILGVQSGOCLSCVGEPTLTLPVNMELYLAKSKSPTFYR RMDGLTSSFSAAYPGWFLCTVBPADQPVRLTQLPENGWNNAPITDVFQCDL"

ORIGIN  
Query Match 99.7%; Score 466.4; DB 11; Length 468;  
Best Local Similarity 99.8%; Pred. No. 4.7e-107;  
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



Db 462 TACCGGGGACATGAGGGCTTACCTCCAGCTTGAAGTGGCTGCTACCCGGGGCTGTT 521  
Qy 360 CTGTGACGAGTGTCTGAAGCCGATCAGCTGTCAAGTCAACCGAGCTTCCGAGAAATGG 419  
Db 522 CTGTGACGAGTGTCTGAAGCCGATCAGCTGTCAAGTCAACCGAGCTTCCGAGAAATGG 581  
Qy 420 TGGCTGGAATGCCCCCATCAAGCTTCTCTTCCAGAGTGAAGTCTAG 468  
Db 582 TGGCTGGAATGCCCCCATCAAGCTTCTCTTCCAGAGTGAAGTCTAG 630  
RESULT 30  
AX675571 480 bp DNA linear PAT 27-MAR-2003  
LOCUS  
DEFINITION Sequence 21 from Patent WO0205704.  
ACCESSION AX675571  
VERSION AX675571.1 GI:29333562  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Padigara, M., Li, L., Zetser, B.D., Casman, S.J., Shenoy, S.,  
Szytek, K.A., Zhong, M., Gangoli, E.A., Burgess, C.E., Paturnian, M.,  
Verne, C.A., Taylor, S., Tcherny, V.T., Miller, C.E., Guo, X.,  
Baldog, F.L., Grose, W.M., Alsbrook, J.P., Gerlach, V.,  
Edingermark, S., Rothenberg, M.E., Ellerman, K., MacDougall, J.,  
Malankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and  
Stone, D.J.  
TITLE Proteins, polynucleotides encoding them and methods of using the  
same  
JOURNAL Patent: WO 0205704-A 21 18-JUL-2002;  
FEATURES  
source Location/Qualifiers  
1. 480  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 75.7%; Score 354.4; DB 6; Length 480;  
Best Local Similarity 85.9%; Pred. No. 9.6e-79;  
Matches 407; Conservative 0; Mismatches 61; Indels 6; Gaps 1;  
Qy 1 ATGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTTGAAGTCTTTAT 60  
Db 1 ATGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTTGAAGTCTTTAT 60  
Qy 61 CTGATATTAACCAAGCTTCTGCTGAGAGGCTGCATGACGAGGAAGTCTATTAAGTGA 120  
Db 61 CTGATATTAACCAAGCTTCTGCTGAGAGGCTGCATGACGAGGAAGTCTATTAAGTGA 120  
Qy 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGTGCAGAGCTGTGCTCCCGTATCTGAGT 180  
Db 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGTGCAGAGCTGTGCTCCCGTATCTGAGT 180  
Qy 121 AAGATCTGATCTTCTTCAAGAGGCTTGGCCCGACCAAGTCTCCCATTTTCTGGGG 180  
Db 121 AAGATCTGATCTTCTTCAAGAGGCTTGGCCCGACCAAGTCTCCCATTTTCTGGGG 180  
Qy 181 GTCCAGGATGAGCCAGTGTCTGTATGTGGGGTGGGGCAGAGCCGATCTTAAC- 238  
Db 181 ATCCAGGAGGAGGAGCCGCTGCTGCTGAGTGTGAGAGAGAGGGGCTTCCCTAAG 240  
Qy 239 - - - - - TAGAGCCAGTGAACATATGAGTCTTATCTTGGTCCAGAGAAATCAAGCTTC 294  
Db 241 CTGAGCAGCGCAGTGAACATATGAGTCTTATCTTGGTCCAGAGAAATCAAGAGCTTC 300  
Qy 295 ACCTTTACCGGCGGAGCATGAGGCTCACTCCAGCTTCAAGTGGGCTGCTTACCCGGGC 354  
Db 301 ACCTTTACCGGCGGAGCATGAGGCTCACTCCAGCTTCAAGTGGGCTGCTTACCCGGGC 360  
Qy 355 TGGTCTCTGTGACAGGTGCTGGAAGCCGATCAGCTGTCAAGTCAACCGAGCTTCCGAG 414

Db 361 TGGTCTCTGTGACAGGTGCTGGAAGCCGATCAGCTGTCAAGTCAACCGAGCTTCCGAG 420  
Qy 415 AATGATGCTGGAATGCCCATCAAGATTTTACTTCCAGAGTGTGACTAG 468  
Db 421 AATGATGCTGGAATGCCCATCAAGATTTTACTTCCAGAGTGTGACTAG 474  
RESULT 31  
AX069335 468 bp DNA linear PAT 25-JAN-2001  
LOCUS  
DEFINITION Sequence 32 from Patent WO0102571.  
ACCESSION AX069335  
VERSION AX069335.1 GI:12579200  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM  
REFERENCE  
AUTHORS Ford, J. and Pace, A.  
TITLE A interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: WO 0102571-A 32 11-JAN-2001;  
FEATURES  
source Location/Qualifiers  
1. 468  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"  
ORIGIN  
Query Match 75.0%; Score 351.2; DB 6; Length 468;  
Best Local Similarity 84.4%; Pred. No. 6.2e-78;  
Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
Qy 1 ATGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTTGAAGTCTTTAT 60  
Db 1 ATGCTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTTGAAGTCTTTAT 60  
Qy 61 CTGATATTAACCAAGCTTCTGCTGAGAGGCTGCATGACGAGGAAGTCTATTAAGTGA 120  
Db 61 CTGATATTAACCAAGCTTCTGCTGAGAGGCTGCATGACGAGGAAGTCTATTAAGTGA 120  
Qy 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGTGCAGAGCTGTGCTCCCGTATCTGAGT 180  
Db 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGTGCAGAGCTGTGCTCCCGTATCTGAGT 180  
Qy 181 GTCCAGGATGAGCCAGTGTCTGTATGTGGGGTGGGGCAGAGCCGATCTTAACACTA 240  
Db 181 GTCCAGGATGAGCCAGTGTCTGTATGTGGGGTGGGGCAGAGCCGATCTTAACACTA 240  
Qy 241 GAGCAGTGAACCATGAGTCTTATCTTGGGCCAAGGAATCCAGAGCTTCACTTC 300  
Db 241 GAGCAGTGAACCATGAGTCTTATCTTGGGCCAAGGAATCCAGAGCTTCACTTC 300  
Qy 301 TACCGGCGGAGCATGAGGCTCACTCCAGCTTGAAGTGGGCTGCTTCCGAGGCTGTTTC 360  
Db 301 TACCGGCGGAGCATGAGGCTCACTCCAGCTTGAAGTGGGCTGCTTCCGAGGCTGTTTC 360  
Qy 361 CTGTGACGAGTGTGCTCCCAATCGGTGAGTGCAGAGCTGTGCTCCCGTATCTGAGT 420  
Db 361 CTGTGACGAGTGTGCTCCCAATCGGTGAGTGCAGAGCTGTGCTCCCGTATCTGAGT 420  
Qy 421 GCGTGAATGCCCATCAAGACTTACTTCCAGAGTGTGACTAG 468  
Db 421 GCGTGAATGCCCATCAAGACTTACTTCCAGAGTGTGACTAG 468  
RESULT 32  
AF230378 471 bp mRNA linear ROD 01-NOV-2001  
LOCUS  
DEFINITION Mus musculus interleukin-1 delta mRNA, complete cds.  
ACCESSION AF230378

VERSION AF230378.1 GI:9651790  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 471)  
 AUTHORS Debetz, R., Timans, J.C., Homey, B., Zurawski, S., Sana, T.R., Lo, S., Wagner, J., Edwards, G., Clifford, T., Memon, S., Bazan, J.F. and Kastelein, R.A.  
 TITLE Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2  
 JOURNAL J. Immunol. 167 (3), 1440-1446 (2001)  
 PUBMED 11466363  
 REFERENCE 2 (bases 1 to 471)  
 AUTHORS Kastelein, R.A., Timans, J.C., Sana, T., Debetz, R. and Bazan, F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-FEB-2000) Molecular Biology, DNAX Research Institute, 901 California Avenue, Palo Alto, CA 94304, USA  
 FEATURES  
 SOURCE  
 1..471  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 1..473  
 /note="IL-1delta; cytokine"  
 /codon\_start=1  
 /product="interleukin-1 delta"  
 /protein\_id="AA91275.1"  
 /db\_xref="GI:9651791"  
 /translation="MNVLSGALCRMKDSALKVYLHNNQLAGLHAERYIKGEISV VPRNADASLSPVILGVGGSGQCSCTEGEPILKPEVIMELYLAKSKSFTFY RDMGLTSSPESAAVPGWFLCTSPBADQPVRLTQIPDPAMDAPITDVFQCCD"  
 ORIGIN  
 Query Match 75.0%; Score 351.2; DB 9; Length 471;  
 Best Local Similarity 84.4%; Pred. No. 6.2e-78;  
 Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
 QY 1 ATGCTCTAGTGGGGGGCTGTGCTCCGAATGAAGACTCGCATGAAGTCTTAT 60  
 DB 4 ATGCTCTAGTGGGGGGCTGTGCTCCGAATGAAGACTCGCATGAAGTCTTAT 63  
 QY 61 CTGCATATAACACGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCAATTAAGTAA 120  
 DB 64 CTGCATATAACACGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCAATTAAGTAA 123  
 QY 121 GAGATCAGCTGTGCTCCCAATCGGTGCTGATGCCAGCTGTCCCGCTCATCTGGGT 180  
 DB 124 GAGATCAGCTGTGCTCCCAATCGGTGCTGATGCCAGCTGTCCCGCTCATCTGGGT 183  
 QY 181 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 240  
 DB 184 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 243  
 QY 241 GAGCAGTGAACATCATGAGCTTATCTTGTGCTCCAGGAATCAAGAGTTCACTTC 300  
 DB 244 GAGCAGTGAACATCATGAGCTTATCTTGTGCTCCAGGAATCAAGAGTTCACTTC 303  
 QY 301 TACCGGGGGGACATGGGGCTCACTCAAGCTTCAAGTGGGTGCTTACCGGGGTGTTTC 360  
 DB 304 TACCGGGGGGACATGGGGCTCACTCAAGCTTCAAGTGGGTGCTTACCGGGGTGTTTC 363  
 QY 361 CTGTGACAGGTGCTGTAAGCCGATCAGCTGTGCAAGTCAACCCAGCTTCCGAGATGAT 420  
 DB 364 CTGTGACAGTCAACCGGAAGTGAACAGCTGTCAAGCTCACTCAAGTCCGAGAGACCC 423  
 QY 421 GAGCTGAATGCCCCCATCAAGACTTCTACTTCAAGAGTGTGACTAG 468  
 DB 424 GAGCTGAATGCCCCCATCAAGACTTCTACTTCAAGAGTGTGACTAG 471

RESULT 33  
 AF200495 1283 bp mRNA linear ROD 11-MAY-2000  
 LOCUS Mus musculus interleukin-1 homolog 3 mRNA, complete cds.  
 DEFINITION AF200495  
 ACCESSION AF200495  
 VERSION AF200495.1 GI:7769117  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1283)  
 AUTHORS Kumar, S., McDonnell, P.C., Lehr, R., Tierney, L., Timans, M.N., Griswold, D.E., Capper, E.A., Tal-Singer, R., Wells, G.I., Doyle, M.L. and Young, P.R.  
 TITLE Identification and initial characterization of four novel members of the interleukin-1 family  
 JOURNAL J. Biol. Chem. 275 (14), 10308-10314 (2000)  
 PUBMED 10744718  
 REFERENCE 2 (bases 1 to 1283)  
 AUTHORS Kumar, S., McDonnell, P.C. and Young, P.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-NOV-1999) Bone and Cartilage Biology, UM 2109, Smithline Beecham Pharmaceuticals, 709 Swedeland Rd., King of Prussia, PA 19406, USA  
 FEATURES  
 SOURCE  
 1..1283  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /dev\_stage="19.5 day embryo"  
 110..577  
 /note="cytokine; IL-13; similar to Homo sapiens IL-13H1 sequence encoded by Genbank Accession Number AF186094"  
 /codon\_start=1  
 /product="interleukin-1 homolog 3"  
 /protein\_id="AA9251.1"  
 /db\_xref="GI:7769118"  
 /translation="MNVLSGALCRMKDSALKVYLHNNQLAGLHAERYIKGEISV VPRNADASLSPVILGVGGSGQCSCTEGEPILKPEVIMELYLAKSKSFTFY RDMGLTSSPESAAVPGWFLCTSPBADQPVRLTQIPDPAMDAPITDVFQCCD"  
 ORIGIN  
 Query Match 75.0%; Score 351.2; DB 9; Length 1283;  
 Best Local Similarity 84.4%; Pred. No. 6e-78;  
 Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
 QY 1 ATGCTCTAGTGGGGGGCTGTGCTCCGAATGAAGACTCGCATGAAGTCTTAT 60  
 DB 110 ATGCTCTAGTGGGGGGCTGTGCTCCGAATGAAGACTCGCATGAAGTCTTAT 169  
 QY 61 CTGCATATAACACGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCAATTAAGTAA 120  
 DB 170 CTGCATATAACACGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCAATTAAGTAA 229  
 QY 171 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 240  
 DB 230 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 289  
 QY 241 GAGCAGTGAACATCATGAGCTTATCTTGTGCTCCAGGAATCAAGAGTTCACTTC 300  
 DB 290 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 349  
 QY 349 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 360  
 DB 350 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 409  
 QY 409 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 420  
 DB 410 GTCCAGAGTGAAGCCAGTGGCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACATA 469

Query 361 CTGTGACGGTGCCTGAGAGCCGATCAGCTGTGACACTCCAGCTTCCGAGAAATGCT 420  
Db 470 CTGTGACCTTCACCGGAAAGCTGACACGACTGTGTACAGGCTTCACTAGATCCCTGAGAACCCC 529  
Qy 421 GCGTGAATGCCCCCATCAGACTTTCTACTTCCAGAGTGTACTAG 468  
Db 530 GCGTGGATGCTCCCATCAGACTTTCTACTTCCAGAGTGTACTAG 577

RESULT 34  
AX080392 1284 bp DNA linear PAT 22-FEB-2001  
LOCUS Definition Sequence 4 from Patent WO0105974.  
AX080392  
VERSION AX080392.1 GI:13159843  
KEYWORDS  
SOURCE Mus sp.  
ORGANISM Mus sp.  
REFERENCE 1. Nicklin, M. and Barton, J.  
AUTHORS The IL-11 gene and polypeptide products  
TITLE Patent: WO 0105974-A 4 25-JAN-2001;  
JOURNAL Interleukin Genetics, Inc. (US)  
FEATURES  
source location/Qualifiers  
1..1284  
/organism="Mus sp."  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10095"

ORIGIN  
Query Match 75.0%; Score 351.2; DB 6; Length 1284;  
Best Local Similarity 84.4%; Pred. No. 6e-78; Indels 0; Gaps 0;  
Matches 395; Conservative 0; Mismatches 73;

1 ATGCTCTGAGTGGGGGCTGTGCTTCCGATGAGAGACTCGGATTTGAAGTCTTTAT 60  
Db 113 ATGCTCTGAGTGGGGGCTGTGCTTCCGATGAGAGACTCGGATTTGAAGTCTTTAT 172  
Qy 61 CTGCAATTAATACCACTTCTTACGTGAGAGGCTGCATGACGAGAAAGTCAATTAAGTGAA 120  
Db 173 CTGCAATTAATACCACTTCTTACGTGAGAGGCTGCATGACGAGAAAGTCAATTAAGTGAG 232  
Qy 121 GAGATCAGCGTGGTCCCAATCGAGTGGTGTGATGCAAGCTGTCCCGATCTGAGGT 180  
Db 233 GAGATCAGTGTGTCCCAATCGAGTGGTGTGATGCAAGCTGTCCCGATCTGAGGT 292  
Qy 181 GTCCAGGATGAGAACCACTGCTGTCAATGTGGGTGGGGGAGAGCCGACTTAACACTA 240  
Db 293 GTTCAAGAGAGAGAACCACTGCTGTCAATGTGGGTGGGGGAGAGCCGACTTAACACTT 352  
Qy 241 GAGCAATGAATCAATCAGAGCTTATCTTGTGTCAGAGAAATCAAGAGTTCACCTTC 300  
Db 353 GAGCAATGAATCAATCAGAGCTTATCTTGTGTCAGAGAAATCAAGAGTTCACCTTC 412  
Qy 301 TACCGGGGAGCATGAGGCTCACTCCAGCTTTCAGTGGTGGTCTACCGGGGCTGAGTTC 360  
Db 413 TACCGGGGAGCATGAGGCTTTCAGCTTCCAGCTTTCAGTGGTGGTCTACCGGGGCTGAGTTC 472  
Qy 361 CTGTGACGAGTGCCTGAGAGCCGATCAGCTGTGACAGACTCAACCAAGCTTCCGAGAAATGCT 420  
Db 473 CTGTGACGAGTGCCTGAGAGCCGATCAGCTGTGACAGACTCAACCAAGCTTCCGAGAAATGCT 532  
Qy 421 GCGTGAATGCCCCCATCAGACTTTCTACTTCCAGAGTGTACTAG 468  
Db 533 GCGTGAATGCCCCCATCAGACTTTCTACTTCCAGAGTGTACTAG 580

RESULT 35  
MMU50429 1284 bp mRNA linear ROD 18-APR-2002  
LOCUS

DEFINITION Mus musculus mRNA for IL-11 protein.  
AJ250429  
VERSION AJ250429.1 GI:6165412  
KEYWORDS IL-11 protein.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1. Barton, J.L., Herbert, R., Bosiaio, D., Higgins, L., and Nicklin, M.J.  
AUTHORS A tissue specific IL-1 receptor antagonist homolog from the IL-1  
TITLE Cluster Jacks IL-1, IL-1a, IL-1b and IL-1c antagonist activities  
JOURNAL Eur. J. Immunol. 30 (11), 3299-3308 (2000)  
PUBMED 11093146  
REFERENCE 2 (bases 1 to 1284)  
AUTHORS Nicklin, M.J.H.  
TITLE Direct Submission  
JOURNAL Submitted (15-OCT-1999) Nicklin, M.J.H., Division of Molecular and  
Genetic Medicine, University of Sheffield, Royal Hallamshire  
Hospital, Sheffield, S10 2JF, UNITED KINGDOM  
COMMENT Related sequence: A1391190.  
FEATURES  
source location/Qualifiers  
1..1284  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE 332733"  
113..580  
/codon\_start=1  
/product="IL-11 protein"  
/protein\_id="CAB59831.1"  
/db\_xref="GI:6165413"  
/db\_xref="GOA:O90Y1"  
/db\_xref="UniProt/Swiss-Prot:O90Y1"  
/translation="MTLSGLCPKMDLSAKVYLHNHNOILAGLHAEXYIKGEISV  
VPRNALDASLPVILVQSSQSLCTSETEGPIKPEVPMELYLKAKSKSTFPR  
RDMGLTSSFEASAVPWFICTSPEDQPVRLTQI PEDPADAPITDFFFOCD"

ORIGIN  
Query Match 75.0%; Score 351.2; DB 9; Length 1284;  
Best Local Similarity 84.4%; Pred. No. 6e-78; Indels 0; Gaps 0;  
Matches 395; Conservative 0; Mismatches 73;

1 ATGCTCTGAGTGGGGGCTGTGCTTCCGATGAGAGACTCGGATTTGAAGTCTTTAT 60  
Db 113 ATGCTCTGAGTGGGGGCTGTGCTTCCGATGAGAGACTCGGATTTGAAGTCTTTAT 172  
Qy 61 CTGCAATTAATACCACTTCTTACGTGAGAGGCTGCATGACGAGAAAGTCAATTAAGTGAA 120  
Db 173 CTGCAATTAATACCACTTCTTACGTGAGAGGCTGCATGACGAGAAAGTCAATTAAGTGAG 232  
Qy 121 GAGATCAGCGTGGTCCCAATCGAGTGGTGTGATGCAAGCTGTCCCGATCTGAGGT 180  
Db 233 GAGATCAGTGTGTCCCAATCGAGTGGTGTGATGCAAGCTGTCCCGATCTGAGGT 292  
Qy 181 GTCCAGGATGAGAACCACTGCTGTCAATGTGGGTGGGGGAGAGCCGACTTAACACTA 240  
Db 293 GTTCAAGAGAGAGAACCACTGCTGTCAATGTGGGTGGGGGAGAGCCGACTTAACACTT 352  
Qy 241 GAGCAATGAATCAATCAGAGCTTATCTTGTGTCAGAGAAATCAAGAGTTCACCTTC 300  
Db 353 GAGCAATGAATCAATCAGAGCTTATCTTGTGTCAGAGAAATCAAGAGTTCACCTTC 412  
Qy 301 TACCGGGGAGCATGAGGCTCACTCCAGCTTTCAGTGGTGGTCTACCGGGGCTGAGTTC 360  
Db 413 TACCGGGGAGCATGAGGCTTTCAGCTTCCAGCTTTCAGTGGTGGTCTACCGGGGCTGAGTTC 472  
Qy 361 CTGTGACGAGTGCCTGAGAGCCGATCAGCTGTGACAGACTCAACCAAGCTTCCGAGAAATGCT 420  
Db 473 CTGTGACGAGTGCCTGAGAGCCGATCAGCTGTGACAGACTCAACCAAGCTTCCGAGAAATGCT 532  
Qy 421 GCGTGAATGCCCCCATCAGACTTTCTACTTCCAGAGTGTACTAG 468

Db 533 GCCTGGATGCTCCATCAGACTTCTACTTTGAGCAGTGTGACTAG 580

RESULT 36  
BD263575 1385 bp DNA linear PAT 17-JUL-2003  
LOCUS BD263575  
DEFINITION IL-1 related polypeptides.  
ACCESSION BD263575.1 GI:33073343  
VERSION BD263575.1  
KEYWORDS JP 200253122-A/9.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1385)  
AUTHORS Goddard, A. and Pan, J.  
TITLE IL-1 related polypeptides  
JOURNAL Patent: JP 200253122-A 9 08-OCT-2002;  
GENENTECH INC  
COMMENT OS Mus musculus (mouse)  
PN JP 200253122-A/9  
PD 08-OCT-2002  
PF 22-DEC-1999 JP 2000591188  
PR 23-DEC-1998 US 60/113430, 22-JAN-1999 US 60/116843 PR  
13-APR-1999 US 60/129122  
PI AUDREY GODDARD, JAMES PAN  
PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12N15/00, C12N5/00  
CC IL-1 related polypeptides  
FH key Location/Qualifiers  
FT source 1..1385  
Location/Qualifiers  
1..1385  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"

ORIGIN  
Query Match 75.0%; Score 351.2; DB 6; Length 1385;  
Best Local Similarity 84.4%; Pred. No. 6e-78;  
Matches 395; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTAAGTCTTTAT 60  
DB 145 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTAAGTCTTTAT 204  
QY 61 CTGCATTAATACCAAGCTTTAGCTGAGAGGCTGCATGCAAGGAAGTCAATTAAGTGAA 120  
DB 205 CTGCACATTAATACCAAGCTTTAGCTGAGAGGCTGCATGCAAGGAAGTCAATTAAGTGAG 264  
QY 121 GAGATCAGCTGTGCCCCCAATCGGTGGTGGATCCAGCCGTGCCCCGTATCTGGGT 180  
DB 265 GAGATCAGCTGTGCCCCCAATCGGTGGTGGATCCAGCCGTGCCCCGTATCTGGGT 324  
QY 181 GTCCAGGAGTGAAGCCAGTGCCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACACTA 240  
DB 325 GTTCAAGAGGAGGAGCCAGTGGCTATCTTGTGGGACAAGAAAGGGCCAATCTGAAACTT 384  
QY 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCAAGAGCTTCACTTC 300  
DB 385 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCAAGAGCTTCACTTC 444  
QY 301 TACCGGCGGAGCATGAGGAGCTCACTCAGAGCTTGAGTGGGCTGCTACCGGGAGTGGTTC 360  
DB 445 TACCGGCGGAGCATGAGGAGCTTCACTCAGAGCTTGAGTGGGCTGCTACCGGGAGTGGTTC 504  
QY 361 CTGTGACGAGTGCCTGAAGCCGATCAGCTGTCAAGACTCAACCAAGCTTCCGAGAAATGAT 420  
DB 505 CTGTGACGAGTGCCTGAAGCCGATCAGCTGTCAAGACTCAACCAAGCTTCCGAGAAATGAT 564

QY 421 GGCTGAATGCCCCATCAGAGACTTCTACTTCCAGAGTGTGACTAG 468  
DB 565 GCCTGGATGCTCCATCAGACTTCTACTTTGAGCAGTGTGACTAG 612

RESULT 37  
BD106430 470 bp DNA linear PAT 18-SEP-2002  
LOCUS BD106430  
DEFINITION Mammalian cytokines, related reagents and methods.  
ACCESSION BD106430  
VERSION BD106430.1 GI:23201248  
KEYWORDS JP 2002501496-A/1.  
SOURCE Chlamydia sp.  
ORGANISM Chlamydia sp.  
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
REFERENCE 1 (bases 1 to 470)  
AUTHORS Hedrick, J.A., Sana, T.R., Bazan, F. and Kastelein, R.A.  
TITLE Mammalian cytokines  
JOURNAL Patent: JP 2002501496-A 1 15-JAN-2002;  
SCHERING CORP  
COMMENT PN JP 2002501496-A/1  
PD 15-JAN-2002  
PF 17-APR-1998 JP 1998546087  
PR 21-APR-1997 US 08/837627, 06-AUG-1997 US 60/055111 PI  
JOSEPH A HEDRICK, THEODORE R SANA, FERNANDO BAZAN, ROBERT A PI  
KASTELEIN  
PC C07K14/545, C07K14/54, C12P21/02, C12N15/12  
CC Strandedness: Single;  
CC Topology: Linear;  
FH key Location/Qualifiers  
FT CDS 1..468.  
Location/Qualifiers  
1..470  
/organism="Chlamydia sp."  
/mol\_type="genomic DNA"  
/db\_xref="taxon:35827"

ORIGIN  
Query Match 74.8%; Score 350.2; DB 6; Length 470;  
Best Local Similarity 84.4%; Pred. No. 1.1e-77;  
Matches 394; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTAAGTCTTTAT 60  
DB 4 ATGGTCTGAGTGGGGGCTGTGCTTCCGAATGAAGACTCGCATTAAGTCTTTAT 63  
QY 61 CTGCATTAATACCAAGCTTTAGCTGAGAGGCTGCATGCAAGGAAGTCAATTAAGTGAA 120  
DB 64 CTGCACATTAATACCAAGCTTTAGCTGAGAGGCTGCATGCAAGGAAGTCAATTAAGTGAG 123  
QY 121 GAGATCAGCTGTGCCCCCAATCGGTGGTGGATCCAGCCGTGCCCCGTATCTGGGT 180  
DB 124 GAGATCAGCTGTGCCCCCAATCGGTGGTGGATCCAGCCGTGCCCCGTATCTGGGT 183  
QY 181 GTCCAGGAGTGAAGCCAGTGCCTGTCAATGTGGGGTGGGGCAGAGCCGACTTAACACTA 240  
DB 184 GTTCAAGAGGAGGAGCCAGTGGCTATCTTGTGGGACAAGAAAGGGCCAATCTGAAACTT 243  
QY 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCAAGAGCTTCACTTC 300  
DB 244 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGTCCAAAGAAATCAAGAGCTTCACTTC 303  
QY 301 TACCGGCGGAGCATGAGGAGCTCACTCAGAGCTTGAGTGGGCTGCTACCGGGAGTGGTTC 360  
DB 304 TACCGGCGGAGCATGAGGAGCTTCACTCAGAGCTTGAGTGGGCTGCTACCGGGAGTGGTTC 363  
QY 361 CTGTGACGAGTGCCTGAAGCCGATCAGCTGTCAAGACTCAACCAAGCTTCCGAGAAATGAT 420  
DB 364 CTGTGACGAGTGCCTGAAGCCGATCAGCTGTCAAGACTCAACCAAGCTTCCGAGAAATGAT 423  
QY 421 GGCTGAATGCCCCATCAGAGACTTCTACTTCCAGAGTGTGACTAG 467

Db 424 GCCTGGGATGCTCCATCAGAGCTTCTACTTTCAGCAGTGTACTA 470

RESULT 38  
AX080399 465 bp DNA linear PAT 22-FEB-2001  
LOCUS AX080399  
DEFINITION Sequence 11 from Patent WO0105974.  
ACCESSION AX080399  
VERSION AX080399.1 GI:13159845  
KEYWORDS  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 Nicklin, M. and Barton, J.  
The 11-111 gene and polypeptide products  
Patent: WO 0105974-A 11-25-JAN-2001;  
JOURNAL Interleukin Genetics, Inc. (US)

FEATURES  
source Location/Qualifiers  
1..465  
/organism="Mus sp."  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10095"

ORIGIN

Query Match 74.4%; Score 348.2; DB 6; Length 465;  
Best Local Similarly 84.3%; Pred. No. 3.5e-77;  
Matches 392; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTAAGAGTCTTAT 60  
Db 1 ATGGTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTAAGAGTCTTAT 60

QY 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCATTAAAGTGAA 120  
Db 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCATTAAAGTGAG 120

QY 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCCCGCTCATCTGGGT 180  
Db 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCCCGCTCATCTGGGC 180

QY 121 GAGATCAGTGTGTCCCAATCGGGCACTGGATCCAGTGTCTCCCTGCATCTGGGC 180  
Db 121 GAGATCAGTGTGTCCCAATCGGGCACTGGATCCAGTGTCTCCCTGCATCTGGGC 180

QY 181 GTCCAGGGTGAAGCCAGCTGTCTGATGTGGGTGGGGCAGAGCCGACTCTAACACTA 240  
Db 181 GTCCAGGGTGAAGCCAGCTGTCTGATGTGGGTGGGGCAGAGCCGACTCTAACACTT 240

QY 181 GTTCAGAGAGAGCCAGCTGTCTTGTGGGACAGAGAAAGGCCAATTTCTGAACTT 240  
Db 181 GTTCAGAGAGAGCCAGCTGTCTTGTGGGACAGAGAAAGGCCAATTTCTGAACTT 240

QY 241 GAGCCAGTGAACATCATGAGCTTATCTTGGTCCAAAGAAATCAAGAGCTTCACTTC 300  
Db 241 GAGCCAGTGAACATCATGAGCTTATCTTGGTCCAAAGAAATCAAGAGCTTCACTTC 300

QY 241 GAGCCAGTGAACATCATGAGCTTATCTTGGTCCAAAGAAATCAAGAGCTTCACTTC 300  
Db 241 GAGCCAGTGAACATCATGAGCTTATCTTGGTCCAAAGAAATCAAGAGCTTCACTTC 300

QY 301 TACCGGGGGGACATGGGGCTCACTCCAGCTTCAAGTGGCTGCTTACCCGGGTGGTTC 360  
Db 301 TACCGGGGGGACATGGGGCTCACTCCAGCTTCAAGTGGCTGCTTACCCGGGTGGTTC 360

QY 301 TACCGGGGGGATATGGGTCTTACTTCAAGCTTCCAGTCCGCTGCTTACCCAGGCTGTTTC 360  
Db 301 TACCGGGGGGATATGGGTCTTACTTCAAGCTTCCAGTCCGCTGCTTACCCAGGCTGTTTC 360

QY 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCACTCAAGCCAGCTTCCGAGAAATGAT 420  
Db 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCACTCAAGCCAGCTTCCGAGAAATGAT 420

QY 361 CTCTGACACTCAACCGAAGCTGACCAAGCTTCTCAGGCTCACTCAAGATCCCTGAGAGACCCC 420  
Db 361 CTCTGACACTCAACCGAAGCTGACCAAGCTTCTCAGGCTCACTCAAGATCCCTGAGAGACCCC 420

QY 421 GCGTGAATGCCCCCATCAGAGCTTCTTACTTCCAGCAGGTGTGAC 465  
Db 421 GCGTGAATGCCCCCATCAGAGCTTCTTACTTCCAGCAGGTGTGAC 465

QY 421 GCGTGGGATGCTCCCATCAGAGCTTCTTACTTCCAGCAGGTGTGAC 465  
Db 421 GCGTGGGATGCTCCCATCAGAGCTTCTTACTTCCAGCAGGTGTGAC 465

RESULT 39  
BD124060 468 bp DNA linear PAT 18-SEP-2002  
LOCUS BD124060  
DEFINITION DNA and polypeptide of IL-1-delta.  
ACCESSION BD124060  
VERSION BD124060.1 GI:23219005  
KEYWORDS JP 200250046-A/1.  
SOURCE Mus musculus (house mouse)

REFERENCE  
AUTHORS Sims, J.B.  
TITLE DNA and polypeptide of IL-1-delta  
JOURNAL Patent: JP 200250046-A 1 08-JAN-2002;  
IMMUNEX CORP  
COMMENT OS Mus musculus (mouse)  
PN JP 200250046-A/1  
PD 08-JAN-2002  
PR 08-JAN-1999 JP 2000527652  
PR 09-JAN-1998 US 60/071074, 01-JUN-1998 US 60/087393 PI  
JOHN ERNEST SIMS  
PC C12N15/09, C07K14/545, C07K16/24, C12N1/19, C12N1/21, C12N5/10, PC  
C12P21/08//  
PC C12M1/00, C12N15/00, C12N5/00  
CC DNA and polypeptide of IL-1-delta  
FH Key Location/Qualifiers  
FT source 1..468  
FT Location/Qualifiers  
1..468  
/organism="Mus musculus (mouse)".

FEATURES  
source Location/Qualifiers  
1..468  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"

ORIGIN

Query Match 74.4%; Score 348.2; DB 6; Length 468;  
Best Local Similarly 84.3%; Pred. No. 3.5e-77;  
Matches 392; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTAAGAGTCTTAT 60  
Db 1 ATGGTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTAAGAGTCTTAT 60

QY 4 ATGGTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTAAGAGTCTTAT 63  
Db 4 ATGGTCTGAGTGGGGGCTGTGCTCCGAATGAAGGCTGGCATTAAGAGTCTTAT 63

QY 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCATTAAAGTGAA 120  
Db 61 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCATTAAAGTGAG 123

QY 64 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCATTAAAGTGAG 123  
Db 64 CTGCATATAACCAAGCTTCTAGCTGAGAGGCTGCATGCAAGGAAGTCATTAAAGTGAG 123

QY 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCCCGCTCATCTGGGT 180  
Db 121 GAGATCAGCTGTGCTCCCAATCGGTGGCTGAGATCCAGCCTGTCCCGCTCATCTGGGC 183

QY 124 GAGATCAGTGTGTCCCAATCGGGCACTGGATCCAGTGTCTCCCTGCATCTGGGC 183  
Db 124 GAGATCAGTGTGTCCCAATCGGGCACTGGATCCAGTGTCTCCCTGCATCTGGGC 183

QY 181 GTCCAGGGTGAAGCCAGCTGTCTGATGTGGGTGGGGCAGAGCCGACTCTAACACTA 240  
Db 181 GTCCAGGGTGAAGCCAGCTGTCTGATGTGGGTGGGGCAGAGCCGACTCTAACACTT 243

QY 184 GTTCAGAGAGAGCCAGCTGTCTTGTGGGACAGAGAAAGGCCAATTTCTGAACTT 243  
Db 184 GTTCAGAGAGAGCCAGCTGTCTTGTGGGACAGAGAAAGGCCAATTTCTGAACTT 243

QY 241 GAGCCAGTGAACATCATGAGCTTATCTTGGTCCAAAGAAATCAAGAGCTTCACTTC 300  
Db 241 GAGCCAGTGAACATCATGAGCTTATCTTGGTCCAAAGAAATCAAGAGCTTCACTTC 303

QY 244 GAGCCAGTGAACATCATGAGCTTATCTTGGTCCAAAGAAATCAAGAGCTTCACTTC 303  
Db 244 GAGCCAGTGAACATCATGAGCTTATCTTGGTCCAAAGAAATCAAGAGCTTCACTTC 303

QY 301 TACCGGGGGGACATGGGGCTCACTCCAGCTTCAAGTGGCTGCTTACCCGGGTGGTTC 360  
Db 301 TACCGGGGGGATATGGGTCTTACTTCAAGCTTCCAGTCCGCTGCTTACCCAGGCTGTTTC 363

QY 304 TACCGGGGGGATATGGGTCTTACTTCAAGCTTCCAGTCCGCTGCTTACCCAGGCTGTTTC 363  
Db 304 TACCGGGGGGATATGGGTCTTACTTCAAGCTTCCAGTCCGCTGCTTACCCAGGCTGTTTC 363

QY 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCACTCAAGCCAGCTTCCGAGAAATGAT 420  
Db 361 CTGTGACAGGTGCTGAGAGCCGATCAGCTGTGCACTCAAGCCAGCTTCCGAGAAATGAT 420

QY 364 CTCTGACACTCAACCGAAGCTGACCAAGCTTCTCAGGCTCACTCAAGATCCCTGAGAGACCCC 423  
Db 364 CTCTGACACTCAACCGAAGCTGACCAAGCTTCTCAGGCTCACTCAAGATCCCTGAGAGACCCC 423

QY 421 GCGTGAATGCCCCCATCAGAGCTTCTTACTTCCAGCAGGTGTGAC 465  
Db 421 GCGTGAATGCCCCCATCAGAGCTTCTTACTTCCAGCAGGTGTGAC 465

QY 424 GCGTGGGATGCTCCCATCAGAGCTTCTTACTTCCAGCAGGTGTGAC 468  
Db 424 GCGTGGGATGCTCCCATCAGAGCTTCTTACTTCCAGCAGGTGTGAC 468

RESULT 40  
BD211432 338 bp DNA linear PAT 17-JUL-2003  
LOCUS BD211432  
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.  
ACCESSION BD211432  
VERSION BD211432.1 GI:33021202  
KEYWORDS JP 2002510492-A/1.  
SOURCE Homo sapiens (human)



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 338)  
AUTHORS Ford, J. and Pace, A.  
TITLE A novel interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: JP 2002510492-A 1 09-APR-2002;  
HYSEQ INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002510492-A/1  
PD 09-APR-2002  
PR 05-APR-1999 JP 2000542457  
PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR  
20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR  
31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR  
11-FEB-1999 US 09/251370  
PI JOHN FORD, ANN PACE  
PC C12N15/09,A61K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,  
PC C12N1/19,  
PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC  
C12N15/00,  
PC A61K37/02,C12N5/00  
CC A novel interleukin-1 receptor antagonist and uses thereof FH  
Key Location/Qualifiers  
FT source 1..338  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source 1..338  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
ORIGIN  
Query Match 51.9%; Score 243; DB 6; Length 338;  
Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 226 CCGACTTAACTAGAGCCAGTGAACATCATGTGAGCTCTATCTTGGTCCCAAGAAATCC 285  
DB 1 CCGACTTAACTAGAGCCAGTGAACATCATGTGAGCTCTATCTTGGTCCCAAGAAATCC 60  
QY 286 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCTCACTTCAGAGTGGGCTGCC 345  
DB 61 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCTCACTTCAGAGTGGGCTGCC 120  
QY 346 TACCCGGGCTGGTTCCTGTGACGCGTCCCTGAAGCCGATCAGCTGTCAAGTCAACCAG 405  
DB 121 TACCCGGGCTGGTTCCTGTGACGCGTCCCTGAAGCCGATCAGCTGTCAAGTCAACCAG 180  
QY 406 CTTCGCCAGAAATGTGGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 465  
DB 181 CTTCGCCAGAAATGTGGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 240  
QY 466 TAG 468  
DB 241 TAG 243  
RESULT 41  
ARI81992 357 bp DNA linear PAT 20-APR-2002  
LOCUS ARI81992  
DEFINITION Sequence 1 from patent US 6337072.  
ACCESSION ARI81992  
VERSION ARI81992.1 GI:20224908  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 357)  
AUTHORS Ford, J. and Pace, A.  
TITLE Interleukin-1 receptor antagonist and recombinant production thereof

JOURNAL Patent: US 6337072-A 1 08-JAN-2002;  
FEATURES location/Qualifiers  
source 1..357  
/organism='unknown'  
/mol\_type='unassigned DNA'  
ORIGIN  
Query Match 51.9%; Score 243; DB 6; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 226 CCGACTTAACTAGAGCCAGTGAACATCATGTGAGCTCTAATCTTGGTCCCAAGAAATCC 285  
DB 1 CCGACTTAACTAGAGCCAGTGAACATCATGTGAGCTCTAATCTTGGTCCCAAGAAATCC 60  
QY 286 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCTCACTTCAGAGTGGGCTGCC 345  
DB 61 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCTCACTTCAGAGTGGGCTGCC 120  
QY 346 TACCCGGGCTGGTTCCTGTGACGCGTCCCTGAAGCCGATCAGCTGTCAAGTCAACCAG 405  
DB 121 TACCCGGGCTGGTTCCTGTGACGCGTCCCTGAAGCCGATCAGCTGTCAAGTCAACCAG 180  
QY 406 CTTCGCCAGAAATGTGGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 465  
DB 181 CTTCGCCAGAAATGTGGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 240  
QY 466 TAG 468  
DB 241 TAG 243

RESULT 42  
AR221126 357 bp DNA linear PAT 26-SEP-2002  
LOCUS AR221126  
DEFINITION Sequence 1 from patent US 6426191.  
ACCESSION AR221126  
VERSION AR221126.1 GI:23328011  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 357)  
AUTHORS Ford, J. and Pace, A.  
TITLE Assays involving an IL-1 receptor antagonist  
JOURNAL Patent: US 6426191-A 1 30-JUL-2002;  
Hyseq, Inc.; Sunnyvale, CA  
FEATURES location/Qualifiers  
source 1..357  
/organism='unknown'  
/mol\_type='genomic DNA'  
ORIGIN  
Query Match 51.9%; Score 243; DB 6; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 226 CCGACTTAACTAGAGCCAGTGAACATCATGTGAGCTCTAATCTTGGTCCCAAGAAATCC 285  
DB 1 CCGACTTAACTAGAGCCAGTGAACATCATGTGAGCTCTAATCTTGGTCCCAAGAAATCC 60  
QY 286 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCTCACTTCAGAGTGGGCTGCC 345  
DB 61 AAGAGCTTCACTTCTACCGGCGGAGCATGAGGCTCTCACTTCAGAGTGGGCTGCC 120  
QY 346 TACCCGGGCTGGTTCCTGTGACGCGTCCCTGAAGCCGATCAGCTGTCAAGTCAACCAG 405  
DB 121 TACCCGGGCTGGTTCCTGTGACGCGTCCCTGAAGCCGATCAGCTGTCAAGTCAACCAG 180  
QY 406 CTTCGCCAGAAATGTGGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 465  
DB 181 CTTCGCCAGAAATGTGGCTGGAATGCCCATCAAGACTTCTAATTCCAGAGTGTGAC 240

Qy 466 TAG 468  
|||  
Db 241 TAG 243

RESULT 43  
AR302954  
LOCUS AR302954 357 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 1 from patent US 6541623.  
ACCESSION AR302954  
VERSION AR302954.1 GI:31691554  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE  
1 (bases 1 to 357)  
FORD, J., HO, A.S.Y. and PACE, A.  
TITLE Interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: US 6541623-A 1 01-APR-2003;  
Hyseq, Inc.; Sunnyvale, CA

FEATURES  
Source Location/Qualifiers  
1..357  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 CCGACTTAACACATGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCAGGAATCC 285  
|||  
Db 1 CCGACTTAACACATGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCAGGAATCC 60

Qy 286 AAGAGCTTCACTTCTACCGCGGAGACATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 345  
|||  
Db 61 AAGAGCTTCACTTCTACCGCGGAGACATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 120

Qy 346 TACCCGGGCTGTTCTCTGACGCTGCAAGCCATCAGCTTCAGCTTCAGCTTCAGCTGCC 405  
|||  
Db 121 TACCCGGGCTGTTCTCTGACGCTGCAAGCCATCAGCTTCAGCTTCAGCTTCAGCTGCC 180

Qy 406 CTTCGCCAGATGCTGCTGGAATGCCCCCATCATCAGACTTCTACTTCAGCACTGTGAC 465  
|||  
Db 181 CTTCGCCAGATGCTGCTGGAATGCCCCCATCATCAGACTTCTACTTCAGCACTGTGAC 240

Qy 466 TAG 468  
|||  
Db 241 TAG 243

RESULT 44  
AX069304 357 bp DNA linear PAT 25-JAN-2001  
LOCUS AX069304  
DEFINITION Sequence 1 from Patent W00102571.  
ACCESSION AX069304  
VERSION AX069304.1 GI:12579176  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1  
FORD, J. and PACE, A.  
TITLE A interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: WO 0102571-A 1 11-JAN-2001;  
HYSEQ, INC. (US)

FEATURES  
Source Location/Qualifiers  
1..357  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

misc\_feature 1..357  
/note="n = A,T,C or G"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e-50;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 CCGACTTAACATGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCAGGAATCC 285  
|||  
Db 1 CCGACTTAACATGAGCCAGTGAACATCATGAGCTCTATCTTGGTCCAGGAATCC 60

Qy 286 AAGAGCTTCACTTCTACCGCGGAGACATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 345  
|||  
Db 61 AAGAGCTTCACTTCTACCGCGGAGACATGAGGCTCACTTCAGCTTCGAGTGGCTGCC 120

Qy 346 TACCCGGGCTGTTCTCTGACGCTGCAAGCCATCAGCTTCAGCTTCAGCTTCAGCTGCC 405  
|||  
Db 121 TACCCGGGCTGTTCTCTGACGCTGCAAGCCATCAGCTTCAGCTTCAGCTTCAGCTGCC 180

Qy 406 CTTCGCCAGATGCTGCTGGAATGCCCCCATCATCAGACTTCTACTTCAGCACTGTGAC 465  
|||  
Db 181 CTTCGCCAGATGCTGCTGGAATGCCCCCATCATCAGACTTCTACTTCAGCACTGTGAC 240

Qy 466 TAG 468  
|||  
Db 241 TAG 243

RESULT 45  
BD211433 985 bp DNA linear PAT 17-JUL-2003  
LOCUS BD211433  
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.  
ACCESSION BD211433  
VERSION BD211433.1 GI:33021203  
KEYWORDS JP 2002510492-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 985)

REFERENCE  
FORD, J. and PACE, A.  
TITLE A novel interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: JP 2002510492-A 2 09-APR-2002;  
HYSEQ INC

COMMENT  
OS Homo sapiens (human)  
PN JP 2002510492-A/2  
PD 09-APR-2002  
PF 05-APR-1999 JP 2000542457  
PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR  
20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR  
31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR  
17-FEB-1999 US 09/251370  
PI JOHN FORD, ANN PACE  
PC C12N15/09, A61K38/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15,  
PC C12N1/19,  
PC C12N1/21, C12N5/10, C07K14/68, G01N33/50, G01N33/566, G01N33/68, PC  
C12N15/00,  
PC A61K37/02, C12N5/00  
CC A novel interleukin-1 receptor antagonist and uses thereof FH  
Key Location/Qualifiers  
FT source 1..985  
/organism="Homo sapiens (human)".

FEATURES  
Source Location/Qualifiers  
1..985  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 51.9%; Score 243; DB 6; Length 985;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;

Matches	243; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	226	CCGACTCTTAAACATAGACCCAGTGAACATCATGAGAGCTTATCTTGTGTGCCAAGAAATCC	285		
Db	1	CCGACTCTTAAACATAGACCCAGTGAACATCATGAGAGCTTATCTTGTGTGCCAAGAAATCC	60		
QY	286	AAGAGCTTACACCTTCTACCGGCGGGACATGAGGGCTCACCTCCAGCTTGTGAGTCCGCTGCC	345		
Db	61	AAGAGCTTACACCTTCTACCGGCGGGACATGAGGGCTCACCTCCAGCTTGTGAGTCCGCTGCC	120		
QY	346	TACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAAGCCTGTGACATCCAG	405		
Db	121	TACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAAGCCTGTGACATCCAG	180		
QY	406	CTTCCCGAAGATGATGCGCTGGAATGCCCATCAACAGCTTCTACTTCAGAGATGTGAC	465		
Db	181	CTTCCCGAAGATGATGCGCTGGAATGCCCATCAACAGCTTCTACTTCAGAGATGTGAC	240		
QY	466	TAG 468			
Db	241	TAG 243			
RESULT 46					
LOCUS	AR181993	985 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	Sequence 2 from patent US 6337072.				
ACCESSION	AR181993				
VERSION	AR181993.1	GI:20224909			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 985)				
AUTHORS	Ford, J. and Pace, A.				
TITLE	Interleukin-1 receptor antagonist and recombinant production thereof				
JOURNAL	Patent: US 6337072-A 2, 08-JAN-2002;				
FEATURES	Location/Qualifiers				
source	1..985				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	51.9%; Score 243; DB 6; Length 985;				
Best Local Similarity	100.0%; Pred. No. 1,3e-50;				
Matches	243; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	226	CCGACTCTTAAACATAGACCCAGTGAACATCATGAGAGCTTATCTTGTGTGCCAAGAAATCC	285		
Db	1	CCGACTCTTAAACATAGACCCAGTGAACATCATGAGAGCTTATCTTGTGTGCCAAGAAATCC	60		
QY	286	AAGAGCTTACACCTTCTACCGGCGGGACATGAGGGCTCACCTCCAGCTTGTGAGTCCGCTGCC	345		
Db	61	AAGAGCTTACACCTTCTACCGGCGGGACATGAGGGCTCACCTCCAGCTTGTGAGTCCGCTGCC	120		
QY	346	TACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAAGCCTGTGACATCCAG	405		
Db	121	TACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAAGCCTGTGACATCCAG	180		
QY	406	CTTCCCGAAGATGATGCGCTGGAATGCCCATCAACAGCTTCTACTTCAGAGATGTGAC	465		
Db	181	CTTCCCGAAGATGATGCGCTGGAATGCCCATCAACAGCTTCTACTTCAGAGATGTGAC	240		
QY	466	TAG 468			
Db	241	TAG 243			
RESULT 47					
LOCUS	AR221127	985 bp	DNA	linear	PAT 26-SEP-2002
DEFINITION	Sequence 2 from patent US 6426191.				

ACCESSION	AR221127	GI:23328012
VERSION	AR221127.1	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 985)	
TITLE	Ford,J. and Pace,A.	
JOURNAL	Assays involving an IL-1 receptor antagonist	
	Patent: US 6426191-A 2 30-JUL-2002;	
FEATURES	Hyseq, Inc.; Sunnyvale, CA	
source	location/Qualifiers	
	1..985	
	/organism="unknown"	
	/mol_type="genomic DNA"	
ORIGIN		
Query Match	51.9%; Score 243; DB 6; Length 985;	
Best Local Similarity	100.0%; Pred. No. 1.3e-50;	
Matches 243; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	226	CCGACTCTTAACACTAGAGCCAGTGAACATCATGTGAGCTCTATCTTGTGCCAAGAAATCC 285
DB	1	CCGACTCTTAACACTAGAGCCAGTGAACATCATGTGAGCTCTATCTTGTGCCAAGAAATCC 60
QY	286	AAGAGCTTCACTTCTTACCCGGCGGACATGCGGCTCACCTTCAGCTTGAATCGGCTGCC 345
DB	61	AAGAGCTTCACTTCTTACCCGGCGGACATGCGGCTCACCTTCAGCTTGAATCGGCTGCC 120
QY	346	TACCCGGGCGTGTCTCGTGTGACGCGTGTGCTGAAGCCGATCAGCCTGTGACCTCACCCAG 405
DB	121	TACCCGGGCGTGTCTCGTGTGACGCGTGTGCTGAAGCCGATCAGCCTGTGACCTCACCCAG 180
QY	406	CTTCCCGAGATGTGTGCTGGAAATGCCCCATCATCAGACTTCTACTTCCAGAGTGTAC 465
DB	181	CTTCCCGAGATGTGTGCTGGAAATGCCCCATCATCAGACTTCTACTTCCAGAGTGTAC 240
QY	466	TAG 468
DB	241	TAG 243
RESULT 48		
LOCUS	AR302955	985 bp DNA linear PAT 12-JUN-2003
DEFINITION	Sequence 2 from patent US 6541623.	
ACCESSION	AR302955	
VERSION	AR302955.1	GI:31691555
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 985)	
TITLE	Ford,J., Ho,A.S.Y. and Pace,A.	
JOURNAL	Interleukin-1 receptor antagonist and uses thereof	
	Patent: US 6541623-A 2 01-APR-2003;	
FEATURES	Hyseq, Inc.; Sunnyvale, CA	
source	location/Qualifiers	
	1..985	
	/organism="unknown"	
	/mol_type="genomic DNA"	
ORIGIN		
Query Match	51.9%; Score 243; DB 6; Length 985;	
Best Local Similarity	100.0%; Pred. No. 1.3e-50;	
Matches 243; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	226	CCGACTCTTAACACTAGAGCCAGTGAACATCATGTGAGCTCTATCTTGTGCCAAGAAATCC 285
DB	1	CCGACTCTTAACACTAGAGCCAGTGAACATCATGTGAGCTCTATCTTGTGCCAAGAAATCC 60
QY	286	AAGAGCTTCACTTCTTACCCGGCGGACATGCGGCTCACCTTCAGCTTGAATCGGCTGCC 345

Db 61 AAGAGCTTACCTTCTACCGGCGGAGATGAGGCTCACTTCACGCTTCGAGTCGGCTGCC 120  
QY 346 TACCCGGGCTGCTTCTCTGTGCACGGTGCTGGAAGCCATCAAGCTGTGCAACTCACCAG 405  
Db 121 TACCCGGGCTGCTTCTCTGTGCACGGTGCTGGAAGCCATCAAGCTGTGCAACTCACCAG 180  
QY 406 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGACTTCTTCTTCCAGCAGTGTGAC 465  
Db 181 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGACTTCTTCTTCCAGCAGTGTGAC 240  
QY 466 TAG 468  
Db 241 TAG 243  
RESULT 49  
AX069305 985 bp DNA linear PAT 25-JAN-2001  
LOCUS  
DEFINITION Sequence 2 from Patent WO0102571.  
ACCESSION AX069305  
VERSION AX069305.1 GI:12579177  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
AUTHORS Ford, J. and Pace, A.  
TITLE A interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: WO 0102571-A 2 11-JAN-2001;  
HYSEQ. INC. (US)  
FEATURES  
Source Location/Qualifiers  
1..985  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
CDS  
1..243  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC27297.1"  
/db\_xref="GI:12579178"  
/translation="PTLTLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAVPM  
FLCTVPEADQPVRLTQLPENGWMAPIITDFYFQCCD"  
ORIGIN  
Query Match 51.9%; Score 243; DB 6; Length 985;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 226 CCGACTTAACACTAGAGCCAGTGAATCATCTGAGCTTATCTTGGTCCCAAGATCC 285  
Db 1 CCGACTTAACACTAGAGCCAGTGAATCATCTGAGCTTATCTTGGTCCCAAGATCC 60  
QY 286 AAGAGCTTACCTTCTACCGGCGGAGATGAGGCTCACTTCACGCTTCGAGTGGCTGCC 345  
Db 61 AAGAGCTTACCTTCTACCGGCGGAGATGAGGCTCACTTCACGCTTCGAGTGGCTGCC 120  
QY 346 TACCCGGGCTGCTTCTCTGTGCACGGTGCTGGAAGCCATCAAGCTGTGCAACTCACCAG 405  
Db 121 TACCCGGGCTGCTTCTCTGTGCACGGTGCTGGAAGCCATCAAGCTGTGCAACTCACCAG 180  
QY 406 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGACTTCTTCTTCCAGCAGTGTGAC 465  
Db 181 CTTCGCCGAGATGGTGGCTGGAATGCCCCATCAAGACTTCTTCTTCCAGCAGTGTGAC 240  
QY 466 TAG 468  
Db 241 TAG 243  
RESULT 50  
BD263574

LOCUS BD263574 295 bp DNA linear PAT 17-JUL-2003  
DEFINITION IL-1 related polypeptides.  
ACCESSION BD263574  
VERSION BD263574.1 GI:33073342  
KEYWORDS JP 2002533122-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
AUTHORS Goddard, A. and Pan, J.  
TITLE IL-1 related polypeptides  
JOURNAL Patent: JP 2002533122-A 8 08-OCT-2002;  
GENENTECH INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002533122-A/8  
PD 08-OCT-2002  
PR 22-DEC-1999 JP 2000591188  
PR 23-DEC-1998 US 60/113430,22-JAN-1999 US 60/116843 PR  
13-APR-1999 US 60/129122  
PI AUREY GODDARD, JAMES PAN  
PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12N15/00, C12N5/00  
CC unknown base  
FH Key Location/Qualifiers  
FT unsure 283.  
FEATURES  
Source Location/Qualifiers  
1..295  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 50.4%; Score 236; DB 6; Length 295;  
Best Local Similarity 99.6%; Pred. No. 8.2e-49;  
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGGTCTGAGTGGGCGCTGTGCTTCCGAATGAAGACCTCCGATGGAAGTGCCTTAT 60  
Db 58 ATGGTCTGAGTGGGCGCTGTGCTTCCGAATGAAGACCTCCGATGGAAGTGCCTTAT 117  
QY 61 CTGCATTAATACAGACTTCTAGCTGAGGCTGCATGCAAGGATCATTTAAAGTGAA 120  
Db 118 CTGCATTAATACAGACTTCTAGCTGAGGCTGCATGCAAGGATCATTTAAAGTGAA 177  
QY 121 GAGATCAGCGTGTGCCCAATCGGTGGCTGATGCGACGCTGTCCCGTCATCTGGGT 180  
Db 178 GAGATCAGCGTGTGCCCAATCGGTGGCTGATGCGACGCTGTCCCGTCATCTGGGT 237  
QY 181 GTCCAGGCTGGAAGCCAGTGCCTGTGATGTTGGGGTGGGGAGAGCCGATCTTACA 237  
Db 238 GTCCAGGCTGGAAGCCAGTGCCTGTGATGTTGGGGTGGGGAGAGCCGATCTTACA 294

Search completed: January 27, 2006, 21:00:29  
Job time : 3030 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: January 27, 2006, 19:03:18 ; Search time 3070 Seconds

(without alignments)  
7132.363 Million cell updates/sec

Title: US-09-612-921B-3

Perfect score: 468

Sequence: 1 atggctcagtgagtgagcgctc.....actccagcagtgagcactag 468

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

1: gb\_eest1:\*  
2: gb\_eest2:\*  
3: gb\_eest3:\*  
4: gb\_eest4:\*  
5: gb\_eest5:\*  
6: gb\_eest6:\*  
7: gb\_eest7:\*  
8: gb\_gsest1:\*  
9: gb\_gsest2:\*  
10: gb\_gsest3:\*  
11: gb\_gsest4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	100.0	468	10	AY413262 Homo sapi
2	468	100.0	762	8	DR004557 TC15434
3	468	100.0	858	2	BI090567 602855674
4	468	100.0	2605	4	CR613851 full-length
5	467.6	99.9	985	4	AL545100 AL545100
6	467	99.8	632	7	CV029389 8151 Full
7	463.2	99.0	468	10	AY413263
8	458	97.9	726	2	BI089828
9	351.2	75.0	1051	4	AK009741
10	351.2	75.0	1199	4	AK008977
11	349.6	74.7	862	6	CB590160
12	343.2	73.3	885	6	CB589411
13	340.8	72.8	2841	4	AK014576
14	338.4	72.3	708	5	BY709379
15	338	72.2	414	7	CR742272
16	333.2	71.2	1531	4	AK010020
17	327	69.9	439	10	AY413264
18	271	57.9	338	5	BK777358
19	258.8	55.5	898	6	CB194288
20	248.2	53.0	691	6	BY754693
21	238.8	51.0	686	5	BY708859
22	208.6	44.6	382	8	W08205

23	166.6	35.6	348	5	BY109350
24	161.6	34.5	343	5	BY107750
25	160	34.2	689	7	CR947864
26	160	34.2	702	7	CR952430
27	153	32.7	689	6	CD368042
28	131	28.0	501	6	CF116914
29	125.2	26.8	621	5	BY714015
30	123.6	26.4	593	6	CD694328
31	111.8	23.9	884	5	BK168482
32	110.6	23.6	470	10	AY402945
33	110.2	23.5	615	7	CR994825
34	110.2	23.5	864	3	BI489807
35	110.2	23.5	1581	4	CR619093
36	110.2	23.5	1644	4	CR616671
37	110.2	23.5	1666	4	CR605915
38	110.2	23.5	735	6	CD468528
39	109	23.3	572	7	CV027812
40	108.6	23.2	757	5	BK424058
41	108.6	23.2	932	5	BK406656
42	108.6	23.2	938	2	BE563703
43	108.6	23.2	955	3	BM009048
44	108.6	23.2	898	1	AL540334
45	108.2	23.1	1069	1	AL554778
46	108.2	23.1	403	3	BM818991
47	107	22.9	640	2	BG288796
48	107	22.9	120	2	BG987216
49	103.8	22.2	435	11	DD043278
50	103.8	22.2	435	11	DD043278
51	103.8	22.2	906	4	AY026753
52	102.2	21.8	970	3	BM921822
53	100.6	21.5	435	11	DD043279
54	100.2	21.4	611	6	CD466328
55	100.2	21.4	640	6	CD466328
56	100.2	21.4	640	6	CD466328
57	100.2	21.4	674	6	CD468330
58	100.2	21.4	726	6	CD469847
59	99.8	21.3	737	3	BI766516
60	99.2	21.2	619	4	AY610257
61	99.2	21.2	685	8	DN381477
62	99.2	21.2	832	3	BI517352
63	99	21.2	671	9	BM959934
64	99	21.2	671	9	BM959934
65	98.6	21.1	526	6	CD471100
66	98.6	21.1	550	6	CD471862
67	98.6	21.1	551	6	CD465665
68	98.6	21.1	552	6	CD471284
69	98.6	21.1	554	6	CD472222
70	98.6	21.1	564	6	CD469052
71	98.6	21.1	574	6	CD468320
72	98.6	21.1	578	6	CD470841
73	98.6	21.1	580	6	CD471738
74	98.6	21.1	581	6	CD465060
75	98.6	21.1	586	6	CD465215
76	98.6	21.1	590	6	CD468534
77	98.6	21.1	591	6	CD465268
78	98.6	21.1	598	6	CD471729
79	98.6	21.1	601	6	CD469756
80	98.6	21.1	602	6	CD465590
81	98.6	21.1	608	6	CD465227
82	98.6	21.1	611	6	CD469122
83	98.6	21.1	611	6	CD465881
84	98.6	21.1	611	6	CD472338
85	98.6	21.1	613	6	CD471113
86	98.6	21.1	616	6	CD465365
87	98.6	21.1	619	6	CD471699
88	98.6	21.1	624	6	CD468325
89	98.6	21.1	626	6	CD469064
90	98.6	21.1	626	6	CD470864
91	98.6	21.1	627	6	CD469704
92	98.6	21.1	627	6	CD469727
93	98.6	21.1	628	6	CD472233
94	98.6	21.1	629	6	CD465892
95	98.6	21.1	630	6	CD469095

BY109350	BY109350
BY107750	BY107750
CR947864	4072568 B
CR952430	4091856 B
CD368042	UI-H-FTI-
CF116914	CH240_401
BY714015	ad97.21 a
CD694328	BY714015
BY708859	EST10851
BK168482	BK168482
AY402945	Homo sapi
CR994825	CR994825
BI489807	603031536
CR619093	full-length
CR616671	full-length
CR605915	full-length
CD468528	Leukos3_3
CV027812	6164 Full1
BK424058	BK424058
BK406656	BK406656
BE563703	601335233
BM009048	603618892
AL540334	AL540334
AL554778	AL554778
BM818991	K-EST0086
BG288796	602388126
BG987216	MR2-HT116
DD043278	Homo sapi
AY026753	Homo sapi
BM921822	AGENCOURT
DD043279	Pan trogl
CD466328	Leukos2_3
CD471267	Leukos5_1
CD469266	Leukos2_2
CD468330	Leukos3_2
CD469847	Leukos2_5
BI766516	603052319
AY610257	Sus scrofa
DN381477	L1B38534
BI517352	603041588
BM959934	BM959934
CJ003758	CJ003758
CD471100	Leukos5_4
CD471862	Leukos5_2
CD465665	Leukos1_6
CD471284	Leukos5_1
CD472222	Leukos6_1
CD469052	Leukos3_2
CD468320	Leukos3_2
CD470841	Leukos5_2
CD471738	Leukos6_4
CD465060	Leukos1_1
CD465215	Leukos1_2
CD468534	Leukos3_3
CD465268	Leukos1_2
CD471729	Leukos6_4
CD469756	Leukos2_8
CD465590	Leukos1_5
CD465227	Leukos1_2
CD469122	Leukos2_1
CD465881	Leukos1_8
CD472338	Leukos5_5
CD471113	Leukos5_4
CD465365	Leukos1_3
CD471699	Leukos6_4
CD468325	Leukos3_4
CD469064	Leukos2_1
CD470864	Leukos2_1
CD469704	Leukos2_8
CD469727	Leukos2_8
CD472233	Leukos6_1
CD465892	Leukos1_8
CD469095	Leukos2_1

96	98.6	21.1	631	6	CD465198	Leukoni_2	169	96	20.5	422	5	BX257557	BX257557
97	98.6	21.1	631	6	CD477123	Leukos5_4	170	96	20.5	493	6	CD465440	CD465440
98	98.6	21.1	632	6	CD465349	Leukoni_3	171	96	20.5	524	6	CD465210	CD465210
99	98.6	21.1	632	6	CD471106	Leukos6_4	172	96	20.5	767	5	BM961605	BM961605
100	98.6	21.1	635	6	CD465263	Leukoni_2	173	96	20.5	787	5	BM957508	BM957508
101	98.6	21.1	635	6	CD470944	Leukos5_3	174	95.8	20.5	397	2	BE846054	BE846054
102	98.6	21.1	637	6	CD468174	Leukos3_1	175	95.6	20.4	635	1	AW262191	AW262191
103	98.6	21.1	637	6	CD469255	Leukos2_2	176	95.6	20.4	747	8	DR423704	DR423704
104	98.6	21.1	638	6	CD465095	Leukoni_1	177	95.6	20.4	1073	1	AL549965	AL549965
105	98.6	21.1	638	6	CD465213	Leukoni_2	178	95.6	20.4	1653	4	CR625646	CR625646
106	98.6	21.1	640	6	CD465088	Leukoni_1	179	95.4	20.4	548	6	CD465466	CD465466
107	98.6	21.1	640	6	CD468221	Leukos3_1	180	95.4	20.4	548	6	CD465688	CD465688
108	98.6	21.1	641	6	CD464253	Leukoni_2	181	95.4	20.4	552	6	CD465571	CD465571
109	98.6	21.1	648	6	CD469258	Leukos2_2	182	95.4	20.4	552	6	CD472212	CD472212
110	98.6	21.1	649	6	CD468208	Leukos3_1	183	95.4	20.4	570	6	CD465471	CD465471
111	98.6	21.1	649	6	CD470680	Leukos4_6	184	95.4	20.4	575	6	CD472063	CD472063
112	98.6	21.1	650	6	CD469384	Leukos3_3	185	95.4	20.4	594	3	BI961215	BI961215
113	98.6	21.1	651	6	CD465603	Leukoni_5	186	95.4	20.4	611	6	CD470551	CD470551
114	98.6	21.1	656	6	CD468855	Leukos3_7	187	95.4	20.4	612	6	CD472073	CD472073
115	98.6	21.1	664	6	CD469738	Leukos2_8	188	95.4	20.4	624	6	CD470145	CD470145
116	98.6	21.1	668	6	CD468509	Leukos3_3	189	95.4	20.4	626	6	CD465027	CD465027
117	98.6	21.1	669	6	CD471103	Leukos5_4	190	95.4	20.4	626	6	CD465898	CD465898
118	98.6	21.1	671	6	CD469212	Leukos2_2	191	95.4	20.4	632	6	CD465780	CD465780
119	98.6	21.1	678	6	CD471002	Leukos5_3	192	95.4	20.4	636	6	CD465368	CD465368
120	98.6	21.1	679	6	CD468654	Leukos3_4	193	95.4	20.4	644	6	CD465445	CD465445
121	98.6	21.1	681	6	CD468234	Leukos3_1	194	95.4	20.4	645	6	CD470695	CD470695
122	98.6	21.1	681	6	CD469261	Leukos3_2	195	95.4	20.4	651	6	CD465206	CD465206
123	98.6	21.1	681	6	CD469556	Leukos2_4	196	95.4	20.4	654	6	CD465899	CD465899
124	98.6	21.1	684	6	CD467302	Leukos1_3	197	95.4	20.4	655	6	CD465350	CD465350
125	98.6	21.1	706	6	CD468361	Leukos3_2	198	95.4	20.4	664	6	CD465547	CD465547
126	98.6	21.1	708	6	CD469842	Leukos2_5	199	95.4	20.4	664	6	CD469431	CD469431
127	98.6	21.1	716	6	CD469857	Leukos2_5	200	95.4	20.4	669	6	CD465595	CD465595
128	98.6	21.1	751	6	CD465904	Leukoni_8	201	95.4	20.4	669	6	CD469577	CD469577
129	98.6	21.1	752	6	CD469744	Leukos2_8	202	95.4	20.4	755	6	CD465555	CD465555
130	98.6	21.1	768	6	CD469568	Leukos2_4	203	95.4	20.4	768	6	CD465034	CD465034
131	98.6	21.1	772	6	CD469830	Leukos2_5	204	95.2	20.3	349	6	CD465356	CD465356
132	98.6	21.1	778	6	CD466354	Leukoni_3	205	95.2	20.3	531	6	CD465907	CD465907
133	98.6	21.1	809	6	CD469371	Leukos2_3	206	95	20.3	432	7	CK615408	CK615408
134	98	20.9	509	3	BP460848	BP460848	207	94.8	20.3	470	10	AY402946	AY402946
135	97.6	20.9	510	6	CD470139	Leukos4_1	208	94.6	20.2	435	8	W78043	W78043
136	97.6	20.9	512	6	CD470313	Leukos4_3	209	94.4	20.2	472	6	CD465371	CD465371
137	97.6	20.9	531	6	AW951593	EST363663	210	94.2	20.1	589	6	CD465072	CD465072
138	97.6	20.9	598	8	DN383540	LIB38534	211	94	20.1	507	7	CD465564	CD465564
139	97.6	20.9	607	6	CD469566	Leukos2_4	212	94	20.1	525	7	CK838069	CK838069
140	97.6	20.9	638	1	AJ746765	Leukos2_4	213	94	20.1	549	2	BE706905	BE706905
141	97.6	20.9	639	1	BP453259	BP453259	214	93.8	20.0	550	6	CD472024	CD472024
142	97.6	20.9	695	3	BP453893	BP453893	215	93.8	20.0	554	6	CD465479	CD465479
143	97.6	20.9	700	3	BP436742	BP436742	216	93.8	20.0	554	6	CD472017	CD472017
144	97.2	20.8	508	6	CD470837	Leukos5_2	217	93.8	20.0	558	6	CD465346	CD465346
145	97	20.7	510	6	CD469536	Leukos2_4	218	93.8	20.0	574	6	CD470105	CD470105
146	97	20.7	510	6	CD471712	Leukos6_4	219	93.8	20.0	657	6	CD465185	CD465185
147	97	20.7	550	6	CD469228	Leukos2_2	220	93.8	20.0	658	1	CD465777	CD465777
148	97	20.7	561	6	CD472084	Leukos6_3	221	93.6	20.0	508	6	AM464284	AM464284
149	97	20.7	571	6	CD468646	Leukos3_4	222	93.6	20.0	536	8	DN440706	DN440706
150	97	20.7	611	6	CD469429	Leukoni_2	223	93.6	20.0	572	8	DN440858	DN440858
151	97	20.7	622	6	CD464241	Leukoni_2	224	93.6	20.0	574	6	CD471928	CD471928
152	97	20.7	632	6	CD470567	Leukos4_5	225	93.6	20.0	694	6	CD465191	CD465191
153	97	20.7	633	6	CD470597	Leukos5_3	226	93.6	20.0	696	6	CD465582	CD465582
154	97	20.7	716	6	CD465601	Leukoni_5	227	93.6	20.0	777	6	CA307607	CA307607
155	97	20.7	732	6	CD465589	Leukoni_5	228	93.4	20.0	487	6	CD471578	CD471578
156	96.8	20.7	454	6	CD470526	Leukos4_5	229	93.2	19.9	533	6	CD472242	CD472242
157	96.8	20.7	473	6	CD465685	Leukoni_6	230	93.2	19.9	545	6	CB466063	CB466063
158	96.8	20.7	529	6	CD469521	Leukos2_4	231	93.2	19.9	648	6	CD465913	CD465913
159	96.8	20.7	546	6	CD466498	Leukoni_2	232	93	19.9	824	3	BI762103	BI762103
160	96.8	20.7	582	6	CD469246	Leukos2_2	233	92.4	19.7	371	2	BI208038	BI208038
161	96.8	20.7	596	6	CD470536	Leukos4_5	234	92.2	19.7	470	10	AY402947	AY402947
162	96.8	20.7	607	6	CD465454	Leukoni_4	235	92.2	19.7	507	7	CD472054	CD472054
163	96.8	20.7	612	6	CD471874	Leukos6_2	236	92.2	19.7	592	8	CK730334	CK730334
164	96.8	20.7	656	6	CD469281	Leukos2_2	237	92.2	19.7	607	7	CD465883	CD465883
165	96.8	20.7	679	6	CD469385	Leukos2_3	238	92.2	19.7	653	5	BY748178	BY748178
166	96.8	20.7	690	6	CD469712	Leukos2_8	239	92.2	19.7	653	5	BY750171	BY750171
167	96.8	20.7	711	6	CD469229	Leukos2_2	240	92.2	19.7	678	5	BY748887	BY748887
168	96.6	20.6	532	6	CD472204	Leukos6_1	241	92.2	19.7	720	5	BY764111	BY764111

242	92.2	19.7	727	5	BY748995	BY748995
243	92.2	19.7	806	4	AK089222	AK089222 Mus muscu
244	92.2	19.7	2456	4	AK076296	AK076296 Mus muscu
245	92	19.7	531	6	CD471875	CD471875 Leukos6_2
246	91.8	19.6	602	6	CD471559	CD471559 Leukos6_6
247	91.4	19.5	705	6	CA309172	CA309172 UI-H-FT1-
248	90.8	19.4	505	6	CD469991	CD469991 Leukos4_2
249	90.8	19.4	507	6	CD465208	CD465208 Leukon1_2
250	90.6	19.4	626	5	BB612586	BB612586 BB612586
251	90.6	19.4	664	5	BY751962	BY751962 BY751962
252	90.6	19.4	1202	2	BG245180	BG245180 602357579
253	90.2	19.3	676	5	BY750355	BY750355 BY750355
254	89.8	19.2	279	6	CD471391	CD471391 Leukos5_5
255	89.8	19.2	653	5	BY750544	BY750544 BY750544
256	89.6	19.1	787	7	CK364274	CK364274 AGENCOURT
257	89	19.0	281	8	RS0241	RS0241 yj58a03.r1
258	89	19.0	532	6	CD464659	CD464659 Leukon4_1
259	88.6	18.9	692	6	CD370507	CD370507 UI-H-FT1-
260	88.6	18.9	693	6	CD368886	CD368886 UI-H-FT1-
261	88	18.8	528	6	CB719487	CB719487 AMGNUNC-N
262	87.6	18.7	260	8	R46871	R46871 yj54f05.r1
263	87.6	18.7	741	6	CA310013	CA310013 UI-H-FT1-
264	87.4	18.7	741	7	CK613932	CK613932 LPSD_H20
265	87	18.6	502	6	CD470412	CD470412 Leukos4_4
266	87	18.6	755	5	BU608443	BU608443 UI-CF-FN0
267	84.2	18.0	690	3	BI912302	BI912302 603069864
268	84	17.9	356	2	BE477245	BE477245 160853_BA
269	84	17.9	371	6	CF116842	CF116842 ad621.z1
270	83.8	17.9	350	2	BI020732	BI020732 CM4-MT021
271	83.2	17.8	490	6	CD464776	CD464776 Leukon4_6
272	82.4	17.5	451	8	DN381876	DN381876 LIB38534
273	81.8	17.6	493	6	CD470570	CD470570 Leukos4_5
274	81.6	17.4	394	10	CE292029	CE292029 tigr-g88-
275	81.6	17.4	730	3	BQ205422	BQ205422 UI-R-DZ1-
276	79.6	17.0	721	3	BQ205443	BQ205443 UI-R-DZ1-
277	79.2	16.9	555	5	CD465205	CD465205 Leukon1_2
278	78.8	16.8	452	6	CD465238	CD465238 Leukon1_2
279	78.8	16.8	482	6	CD469057	CD469057 Leukos2_1
280	78.6	16.8	459	6	CD472028	CD472028 Leukos6_3
281	78.6	16.8	491	6	CD471860	CD471860 Leukos6_2
282	77.8	16.6	455	6	CD465352	CD465352 Leukon1_3
283	77.8	16.6	474	6	CD471426	CD471426 Leukos5_5
284	77.4	16.5	489	6	CD469108	CD469108 Leukos2_1
285	77.4	16.5	862	7	CK466952	CK466952 938212_Ma
286	76.8	16.4	477	6	CD465713	CD465713 Leukon1_6
287	76.8	16.4	666	2	BG698522	BG698522 602658501
288	76.6	16.4	638	3	BM929618	BM929618 UI-E-EJ1-
289	75.4	16.1	359	6	CD469642	CD469642 Leukos2_7
290	75.4	16.1	473	6	CD465545	CD465545 Leukon1_5
291	74.8	16.0	811	5	BU247129	BU247129 603782910
292	73	15.6	364	7	CK607331	CK607331 Control6
293	72.4	15.5	474	6	CD472079	CD472079 Leukos6_3
294	71.8	15.3	476	6	CD465816	CD465816 Leukon1_7
295	71.4	15.3	470	6	CD471927	CD471927 Leukos6_2
296	70.4	15.0	446	6	CD465041	CD465041 Leukon1_1
297	70.4	15.0	469	6	CD470409	CD470409 Leukos4_4
298	70	15.0	488	5	BX280976	BX280976 BX280976
299	69.4	14.8	420	6	CD468372	CD468372 Leukos3_2
300	66.8	14.3	976	2	BE563442	BE563442 601335496

## ALIGNMENTS

RESULT 1	AY413262	468 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY413262				
DEFINITION	Homo sapiens IL1F5 gene, VIRUTAL TRANSCRIPT, partial sequence.				
ACCESSION	AY413262				
VERSION	AY413262.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
AUTHORS	1 (bases 1 to 468) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Interfing nonneutral evolution from human-chimp-mouse orthologous gene tios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
REFERENCE	14671302 2 (bases 1 to 468) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.
AUTHORS	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1..468 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>468 /gene="IL1F5" /locus_tag="HCM4832"
gene	
ORIGIN	
Query Match	100.0%; Score 468; DB 10; Length 468;
Best Local Similarity	100.0%; Pred. No. 1.5e-118;
Matches	468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1	ATGGTCCCTAGGCGGCGCTGCTCCGAATGAAGAGCTGGCATTAAGGCTTTAT 60
1	ATGGTCCCTAGGCGGCGCTGCTCCGAATGAAGAGCTGGCATTAAGGCTTTAT 60
61	CTGCATTAATACAGCTTCTAGCTGAGGCTGATGACGAGGAGGCTTAAGGTGA 120
61	CTGCATTAATACAGCTTCTAGCTGAGGCTGATGACGAGGAGGCTTAAGGTGA 120
121	GAGATCAGCTGCTCCCAATGCTGATGCCAGCTGCTCCCTCATCTGGGT 180
121	GAGATCAGCTGCTCCCAATGCTGATGCCAGCTGCTCCCTCATCTGGGT 180
181	GTCGAGGCTGGAAGCAGTCCCTGTCATGTTGGGGGCGGAGGCGGCTTAACATA 240
181	GTCGAGGCTGGAAGCAGTCCCTGTCATGTTGGGGGCGGAGGCGGCTTAACATA 240
241	GAGCAGTGAACATATGAGCTCTATCTTGTGCAAGAAATCAAGAGTTCACTTC 300
241	GAGCAGTGAACATATGAGCTCTATCTTGTGCAAGAAATCAAGAGTTCACTTC 300
301	TACCGGCGGAGCATGAGGCTCACTTCAGCTTGAAGTGGCTGCTTACCGGCTGCTTC 360
301	TACCGGCGGAGCATGAGGCTCACTTCAGCTTGAAGTGGCTGCTTACCGGCTGCTTC 360
361	CTGTGACAGCTGCTGGAAGCGATGAGCTGTCAGCTCAACCAAGTTCCAGAAATG 420
361	CTGTGACAGCTGCTGGAAGCGATGAGCTGTCAGCTCAACCAAGTTCCAGAAATG 420
421	GGCTGAATGCCCCATCAAGACTTCTTCACTTCAGAGAGTGTAGTAG 468
421	GGCTGAATGCCCCATCAAGACTTCTTCACTTCAGAGAGTGTAGTAG 468

RESULT 2	DR004557	762 bp	mRNA	linear	EST 17-MAY-2005
LOCUS	DR004557				

DEFINITION	TC115434 Human placenta, large insert, pcMV expression library Homo sapiens cDNA clone TC115434 5', similar to Homo sapiens interluc1in 1 family, member 5 (delta) (IL1F5), transcript variant 1, mRNA sequence.			
ACCESSION	DR004557.1	GI:66264430		
VERSION	DR004557			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.			
AUTHORS	1 (bases 1 to 762)			
TITLE	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Yag,G. and He,W.			
JOURNAL	High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts			
COMMENT	Unpublished (2005)			
	Contact: Kovacs, KF			
	High throughput cDNA Cloning			
	Origene Technologies, Inc. ( www.origene.com )			
	6 Taft Court, Suite 100, Rockville, MD 20850, USA			
	Tel: 301 340 3188			
	Fax: 301 340 8606			
	Email: cDNA@origene.com			
	This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc.			
	Please contact Origene for access.			
	Origene Technologies, Inc.			
	6 Taft Ct. Suite 100			
	Rockville, MD 20850			
	Tel: (301) 340-3188			
	http://www.origene.com			
	Seq primer: PCMV6 5prime forward vector primer, Origene Technologies Inc.			
FEATURES	Location/Qualifiers			
source	1..762			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="TC115434"			
	/issue_type="Placenta"			
	/clone_lib="Human placenta, large insert, pcMV expression library"			
	/note="Vector: pCMV6-XL4; Site_1: EcoRI; Site_2: Xho1/Sall1 compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcript; cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"			
ORIGIN				
Query Match	100.0%;	Score 468;	DB 8;	Length 762;
Best Local Similarity	100.0%;	Pred. No. 1,7e-118;		
Matches	468;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps	0;
OY	1	ATGGTCCTAGAGGGGCGCTGCTTCCGATGAAGAACTCGGCATTGAAGTGCTTTAT	60	
DB	69	ATGGTCCTAGAGGGGCGCTGCTTCCGATGAAGAACTCGGCATTGAAGTGCTTTAT	128	
OY	61	CTGCATTAATTAACAGCTTTAGCTGGAGGGCTGCATGCAGGAGAGGCTATTAAAGTGAA	120	
DB	129	CTGCATTAATTAACAGCTTTAGCTGGAGGGCTGCATGCAGGAGAGGCTATTAAAGTGAA	188	
OY	121	GAGATCAGCGTGTCTCCCAATGGTGATGCCAGCCTGTCCCGCTATCTTGGGT	180	
DB	189	GAGATCAGCGTGTCTCCCAATGGTGATGCCAGCCTGTCCCGCTATCTTGGGT	248	
OY	181	GTCCAGGGGTGAAAGCCAGTGCCTGTCATGTGGGGTGGGCAAGAGCCGACTTAACACTA	240	
DB	249	GTCCAGGGGTGAAAGCCAGTGCCTGTCATGTGGGGTGGGCAAGAGCCGACTTAACACTA	308	

Oy		241	GAGCAGGAAACATCATGTAGACTCTATCTTGGTGCCAGAAGATCCAAAGCTTCACCTTC	300
Db		309	GAGGCAGGAACATCATGTAGACTCTATCTTGGTGCCAGAAGATCCAAAGCTTCACCTTC	368
Oy		301	TACCGGCGGGGCATATGGGGCTCACTCCAGCTTCGATCGGCTGCCCTAACCGGGCTGGTTC	360
Db		369	TACCGGGGGGACATGGGGCTCACCTCCAGCTTCGATCGGCTGCCCTAACCGGGCTGGTTC	428
Oy		361	CTGTGCACAGGTGCTGGAAGCCGATTAAGCTGTGCACAATCCACAGTTTCCGAGAATGGT	420
Db		429	CTGTGCACAGGTGCTGGAAGCCGATTAAGCTGTGCACAATCCACAGTTTCCGAGAATGGT	488
Oy		421	GGCTGGAAATCCCCCATCACAGACTTCTACTTCCAGCAGTGTAGTAG	468
Db		489	GGCTGGAAATCCCCCATCACAGACTTCTACTTCCAGCAGTGTAGTAGTAG	536
RESULT_3				
B1090567				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
Oy				
Db				
Oy				
Db				



Qy 121 GAGATCAGCGTGTGCTCCCAATCGTGTGATGATGACAGCTGTGCTCCCGCTCATCTGGGT 180  
Db 255 GAGATCAGCGTGTGCTCCCAATCGTGTGATGATGACAGCTGTGCTCCCGCTCATCTGGGT 314  
Qy 181 GTCCAGGGGTGGAAGCCAGTGTCTGATGTGGGGGTGGGGCAGAGCCGACTTAACACTA 240  
Db 315 GTCCAGGGGTGGAAGCCAGTGTCTGATGTGGGGGTGGGGCAGAGCCGACTTAACACTA 374  
Qy 241 GAGCAGGGAATCATATGAGAGCTCTATCTTGTGGCCAGGAATCCAGAGCTTCACTTC 300  
Db 375 GAGCAGGGAATCATATGAGAGCTCTATCTTGTGGCCAGGAATCCAGAGCTTCACTTC 434  
Qy 301 TACCGGCGGGAATCATATGAGAGCTCTATCTTGTGGCCAGGAATCCAGAGCTTCACTTC 360  
Db 435 TACCGGCGGGAATCATATGAGAGCTCTATCTTGTGGCCAGGAATCCAGAGCTTCACTTC 494  
Qy 361 CTGTGACGCGTGTGCTGGAAGCCGATGAGCTGTGATGATGATGATGATGATGATGATGAT 420  
Db 495 CTGTGACGCGTGTGCTGGAAGCCGATGAGCTGTGATGATGATGATGATGATGATGATGAT 554  
Qy 421 GGCTGGAAATGCCCATCAAGAGCTTCACTTCCAGAGCTGTGACTAG 468  
Db 555 GGCTGGAAATGCCCATCAAGAGCTTCACTTCCAGAGCTGTGACTAG 602

RESULT 4  
LOCUS CR613851 2605 bp mRNA linear HTC 21-JUL-2004  
DEFINITION Full-length cDNA clone CSOD1013YA07 of Placenta Cot 25-normalized  
ACCESSION CR613851  
VERSION CR613851.1 GI:50494658  
KEYWORDS HTC; cDNA; cDNA; cDNA  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 2605)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact: Feng Liang Email: fliang@life.rockefeller.edu  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Parade Avenue  
2 (bases 1 to 2605)  
REFERENCE 2 (bases 1 to 2605)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry-Cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)  
COMMENT - Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
FEATURES  
Location/Qualifiers  
1..2605  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1013YA07"  
/cissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

ORIGIN  
Query Match 100.0%; Score 468; DB 4; Length 2605;  
Best Local Similarity 100.0%; Pred. No. 2.1e-118; Indels 0; Gaps 0;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCTCTGAGTGGGCGCTGTGCTTCCGAATGAAGACTCGGCAATGAAGTGGCTTAT 60  
Db 103 ATGCTCTGAGTGGGCGCTGTGCTTCCGAATGAAGACTCGGCAATGAAGTGGCTTAT 162

Qy 61 CTGCATTAATACAGCTTCTAGCTGAGGGCTGCATGACAGGGAAGTCTAATAAGTGA 120  
Db 163 CTGCATTAATACAGCTTCTAGCTGAGGGCTGCATGACAGGGAAGTCTAATAAGTGA 222  
Qy 121 GAGATCAGCGTGTGCTCCCAATCGTGTGATGATGACAGCTGTGCTCCCGCTCATCTGGGT 180  
Db 223 GAGATCAGCGTGTGCTCCCAATCGTGTGATGATGACAGCTGTGCTCCCGCTCATCTGGGT 282  
Qy 181 GTCCAGGGGTGGAAGCCAGTGTCTGATGTGGGGGTGGGGCAGAGCCGACTTAACACTA 240  
Db 283 GTCCAGGGGTGGAAGCCAGTGTCTGATGTGGGGGTGGGGCAGAGCCGACTTAACACTA 342  
Qy 241 GAGCAGGGAATCATATGAGAGCTCTATCTTGTGGCCAGGAATCCAGAGCTTCACTTC 300  
Db 343 GAGCAGGGAATCATATGAGAGCTCTATCTTGTGGCCAGGAATCCAGAGCTTCACTTC 402  
Qy 301 TACCGGCGGGAATCATATGAGAGCTCTATCTTGTGGCCAGGAATCCAGAGCTTCACTTC 360  
Db 403 TACCGGCGGGAATCATATGAGAGCTCTATCTTGTGGCCAGGAATCCAGAGCTTCACTTC 462  
Qy 361 CTGTGACGCGTGTGCTGGAAGCCGATGAGCTGTGATGATGATGATGATGATGATGATGAT 420  
Db 463 CTGTGACGCGTGTGCTGGAAGCCGATGAGCTGTGATGATGATGATGATGATGATGATGAT 522  
Qy 421 GGCTGGAAATGCCCATCAAGAGCTTCACTTCCAGAGCTGTGACTAG 468  
Db 523 GGCTGGAAATGCCCATCAAGAGCTTCACTTCCAGAGCTGTGACTAG 570

RESULT 5  
LOCUS AL545100 985 bp mRNA linear EST 25-MAR-2004  
DEFINITION AL545100 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
ACCESSION AL545100  
VERSION AL545100.3 GI:45745585  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 985)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
REMARK On Feb 15, 2001 this sequence version replaced gi:31266936.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE  
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1383.f.  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CSOD1013YA04QP1c=1383.f.  
FEATURES  
Location/Qualifiers  
1..985  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1013YA07"  
/cissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_id="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 99.8%; Score 467.6; DB 1; Length 985;  
 Best Local Similarity 99.8%; Pred. No. 2.3e-118;  
 Matches 467; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGTCCTGAGTGGGGGCTGTGCTTCCGAAATGAAGCACTGGCATTAAGTGTCTTAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 103 ATGGCTCTKAGTGGGGGCTGTGCTTCCGAAATGAAGCACTGGCATTAAGTGTCTTAT 162
QY 61 CTGCATATAACCAAGCTTCTAGCTGAGGGCTGCATGAGGGAAGTCATTAAAGTGA 120
DB 163 CTGCATATAACCAAGCTTCTAGCTGAGGGCTGCATGAGGGAAGTCATTAAAGTGA 222
QY 121 GAGATCAGCTGTGCTCCCAATTCGTGCTGATGCGACCTGTCCCGCATCTGTGGT 180
DB 223 GAGATCAGCTGTGCTCCCAATTCGTGCTGATGCGACCTGTCCCGCATCTGTGGT 282
QY 181 GTCCAGGGTGAAGCAGTGCCTGTCTATGTGGGGTGGGGCAGAGCCGACTTAACACTA 240
DB 283 GTCCAGGGTGAAGCAGTGCCTGTCTATGTGGGGTGGGGCAGAGCCGACTTAACACTA 342
QY 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGCGAAGAAATCCAGAGCTTCACTTC 300
DB 343 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGCGAAGAAATCCAGAGCTTCACTTC 402
QY 301 TACCGCGGGACATGAGGGCTCACTCCAGCTTCAAGTGGCTCTACCCGGCTGTTC 360
DB 403 TACCGCGGGACATGAGGGCTCACTCCAGCTTCAAGTGGCTCTACCCGGCTGTTC 462
QY 361 CTGTCACGCTGTGCTGAGAGCCGATCAGCTGTCACTCACTCACTCCAGCTTCCAGAGATGT 420
DB 463 CTGTCACGCTGTGCTGAGAGCCGATCAGCTGTCACTCACTCACTCCAGCTTCCAGAGATGT 522
QY 421 GGCTGGAATGCCCCCATCAAGACTTCTTCACTTCCAGAGTGTACTAG 468
DB 523 GGCTGGAATGCCCCCATCAAGACTTCTTCACTTCCAGAGTGTACTAG 570

```

RESULT 6  
 CVO29389 632 bp mRNA linear EST 20-AUG-2004  
 LOCUS sapiens cDNA 5' similar to BC024747, mRNA sequence.

ACCESSION CVO29389.1 GI:51487548  
 VERSION CVO29389.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 632)

REFERENCE  
 AUTHORS Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,  
 Driscoll,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,  
 Clingingsmith,T.R., Hartley,J.L., Espósito,D., Cheo,D., Moore,T.,  
 Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Pouch,C.,  
 Vandenneute,J., Chisick,M.E., Albaladejo,S., Hill,D.E. and Vidal,M.  
 Human ORFeome Version 1.1: a Platform for Reverse Proteomics  
 Genome Res. (2004) In press

TITLE  
 JOURNAL COMMENT Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739  
 Email: Marc.Vidal@dfci.harvard.edu  
 ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF  
 results from a PCR reaction using an MGC full-length cDNA as  
 template DNA and ORF specific primers  
 PCR Primers  
 FORWARD: ATGTCCTGAGTGGGGGCT  
 BACKWARD: TAGTCACAGCTGGAAGTAGAA  
 Insert Length: 632 Std Error: 45.00

Plate: 11027 row: 10 column: F  
 Seq primer: ACTGGCGGTGTTTACACAGCTGCTGACTGGAAAC  
 High quality sequence start: 99  
 High quality sequence stop: 631  
 POLYA=No.

## FEATURES

source Location/Qualifiers  
 1..632  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="mixed"  
 /clone\_id="Full Length cDNA from the Mammalian Gene  
 Collection"  
 /note="Vector: mixed; The ORFs were PCR amplified from the  
 MGC (Mammalian Gene Collection) as of April 2004 and  
 cloned by recombinational Gateway cloning into pDONR223  
 Donor vector. Reference: MGC (Mammalian Gene Collection)  
 Program Team, Generation and Initial Analysis of more than  
 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,  
 2002, 99(26), 16899-16903"

## ORIGIN

Query Match 99.8%; Score 467; DB 7; Length 632;  
 Best Local Similarity 100.0%; Pred. No. 3e-118;  
 Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGTCCTGAGTGGGGGCTGTGCTTCCGAAATGAAGCACTGGCATTAAGTGTCTTAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 ATGGCTCTKAGTGGGGGCTGTGCTTCCGAAATGAAGCACTGGCATTAAGTGTCTTAT 60
QY 61 CTGCATATAACCAAGCTTCTAGCTGAGGGCTGCATGAGGGAAGTCATTAAAGTGA 120
DB 61 CTGCATATAACCAAGCTTCTAGCTGAGGGCTGCATGAGGGAAGTCATTAAAGTGA 120
QY 121 GAGATCAGCTGTGCTCCCAATTCGTGCTGATGCGACCTGTCCCGCATCTGTGGT 180
DB 121 GAGATCAGCTGTGCTCCCAATTCGTGCTGATGCGACCTGTCCCGCATCTGTGGT 180
QY 181 GTCCAGGGTGAAGCAGTGCCTGTCTATGTGGGGTGGGGCAGAGCCGACTTAACACTA 240
DB 181 GTCCAGGGTGAAGCAGTGCCTGTCTATGTGGGGTGGGGCAGAGCCGACTTAACACTA 240
QY 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGCGAAGAAATCCAGAGCTTCACTTC 300
DB 241 GAGCCAGTGAACATCATGAGAGCTTATCTTGTGCGAAGAAATCCAGAGCTTCACTTC 300
QY 301 TACCGCGGGACATGAGGGCTCACTCCAGCTTCAAGTGGCTCTACCCGGCTGTTC 360
DB 301 TACCGCGGGACATGAGGGCTCACTCCAGCTTCAAGTGGCTCTACCCGGCTGTTC 360
QY 361 CTGTCACGCTGTGCTGAGAGCCGATCAGCTGTCACTCACTCACTCCAGCTTCCAGAGATGT 420
DB 361 CTGTCACGCTGTGCTGAGAGCCGATCAGCTGTCACTCACTCACTCCAGCTTCCAGAGATGT 420
QY 421 GGCTGGAATGCCCCCATCAAGACTTCTTCACTTCCAGAGTGTACTAG 467
DB 421 GGCTGGAATGCCCCCATCAAGACTTCTTCACTTCCAGAGTGTACTAG 467

```

RESULT 7  
 AY413263 468 bp DNA linear GSS 17-DEC-2003  
 LOCUS Pan troglodytes IL15 gene, VIRUAL TRANSCRIPT, partial sequence.  
 DEFINITION genomic survey sequence.  
 ACCESSION AY413263  
 VERSION AY413263.1 GI:39769225  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Pan.  
 1 (bases 1 to 468)

AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene titers

JOURNAL Science 302 (5652), 1960-1963 (2003)

REFERENCE 14671302

AUTHORS 2 (bases 1 to 468)

TITLE Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source 1..468

organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

<1..>468

/gene="IL1F5"

/locus\_tag="HCM4832"

ORIGIN

Query Match 99.0%; Score 463.2; DB 10; Length 468;

Best Local Similarity 99.4%; Pred. No. 3.2e-117;

Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGTCCTGAGTGGGGCGCTGCTGCTCCGAATGAAGAAGTCCGAGCTTGAAGTCTTAT 60

DB 1 ATGGTCCTGAGTGGGGCGCTGCTGCTCCGAATGAAGAAGTCCGAGCTTGAAGTCTTAT 60

QY 61 CTGCATTAATTAACAGCTTCTAGCTGAGAGGCTGATGACAGGAAGTCAATTAAGGTGA 120

DB 61 CTGCATTAATTAACAGCTTCTAGCTGAGAGGCTGATGACAGGAAGTCAATTAAGGTGA 120

QY 121 GAGATCAGCTGTGCTCCCAATCGTGTGCTGATGCCAGCTGTCCCGCTCATCTGGGT 180

DB 121 GAGATCAGCTGTGCTCCCAATCGTGTGCTGATGCCAGCTGTCCCGCTCATCTGGGT 180

QY 121 GAGATCAGCTGTGCTCCCAATCGTGTGCTGATGCCAGCTGTCCCGCTCATCTGGGT 180

DB 121 GAGATCAGCTGTGCTCCCAATCGTGTGCTGATGCCAGCTGTCCCGCTCATCTGGGT 180

QY 181 GTCCAGGGGTGAAGCAGTGCCTGTCATGTGAGGGCGGGCAGAGCCGACTTAACACTA 240

DB 181 GTCCAGGGGTGAAGCAGTGCCTGTCATGTGAGGGCGGGCAGAGCCGACTTAACACTA 240

QY 241 GAGCAGTGAACATCATGAGCTTATCTTGGTGCCAAAGAAATCCAGAGCTTCACTTC 300

DB 241 GAGCAGTGAACATCATGAGCTTATCTTGGTGCCAAAGAAATCCAGAGCTTCACTTC 300

QY 301 TACCGGCGGAGCATGGGGCTCACTTCAGCTTGAAGTGGCTTACCCGGGGCTGGTTC 360

DB 301 TACCGGCGGAGCATGGGGCTCACTTCAGCTTGAAGTGGCTTACCCGGGGCTGGTTC 360

QY 361 CTGTCCAGCGTGTGCTGAAGCCGATCAGCTGTCAACTCACTCAAGTTCCTCCAGATGT 420

DB 361 CTGTCCAGCGTGTGCTGAAGCCGATCAGCTGTCAACTCACTCAAGTTCCTCCAGATGT 420

QY 421 GGCTGGAATGCCCATCAAGACTTTCTTCTCCAGAGTGTGACTAG 468

DB 421 GGCTGGAATGCCCATCAAGACTTTCTTCTCCAGAGTGTGACTAG 468

RESULT 8

LOCUS B1089828 726 bp mRNA linear EST 20-JUN-2001

DEFINITION 602855071P1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:4996432 5'

ACCESSION B1089828

VERSION B1089828.1 GI:14508158

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 726)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLM11021 row: n column: 17  
High quality sequence stop: 709.

FEATURES

source 1..726

organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4996432"

/cell\_line="MGC36"

/lab\_host="DH10B"

/clone\_11b="NIH\_MGC\_10"

/note="Organ: cervix; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 Kb. Library prepared by Life Technologies."

ORIGIN

Query Match 97.9%; Score 458; DB 2; Length 726;

Best Local Similarity 100.0%; Pred. No. 9.7e-116;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GTGGGGCGCTGTGCTTCCGAATGAAGAAGTCCGAGCTTGAAGTCTTATTCGATATA 70

DB 1 GTGGGGCGCTGTGCTTCCGAATGAAGAAGTCCGAGCTTGAAGTCTTATTCGATATA 70

QY 71 ACCAGCTTCTAGCTGAGAGGCTGCATGCAGGAGGAGTCAATTAAGGTGAAGATCAGG 130

DB 71 ACCAGCTTCTAGCTGAGAGGCTGCATGCAGGAGGAGTCAATTAAGGTGAAGATCAGG 130

QY 61 ACCAGCTTCTAGCTGAGAGGCTGCATGCAGGAGGAGTCAATTAAGGTGAAGATCAGG 120

DB 61 ACCAGCTTCTAGCTGAGAGGCTGCATGCAGGAGGAGTCAATTAAGGTGAAGATCAGG 120

QY 131 TGGTCCCAATCGTGTGCTGATGTCAGAGCTTCCCGCTCATCTGGGTGTCCAGGGTG 190

DB 131 TGGTCCCAATCGTGTGCTGATGTCAGAGCTTCCCGCTCATCTGGGTGTCCAGGGTG 190

QY 121 TGGTCCCAATCGTGTGCTGATGTCAGAGCTTCCCGCTCATCTGGGTGTCCAGGGTG 180

DB 121 TGGTCCCAATCGTGTGCTGATGTCAGAGCTTCCCGCTCATCTGGGTGTCCAGGGTG 180

QY 191 GAAGCAGTGTCTGATGTGGGGGTGGGGCAGAGCCGACTTAACACTAGAGCCAGTGA 250

DB 191 GAAGCAGTGTCTGATGTGGGGGTGGGGCAGAGCCGACTTAACACTAGAGCCAGTGA 250

QY 241 GAGCAGTGAACATCATGAGCTTATCTTGGTGCCAAAGAAATCCAGAGCTTCACTTC 300

DB 241 GAGCAGTGAACATCATGAGCTTATCTTGGTGCCAAAGAAATCCAGAGCTTCACTTC 300

QY 301 TACCGGCGGAGCATGGGGCTCACTTCAGCTTGAAGTGGCTTACCCGGGGCTGGTTC 360

DB 301 TACCGGCGGAGCATGGGGCTCACTTCAGCTTGAAGTGGCTTACCCGGGGCTGGTTC 360

QY 371 TGGCTGAAGCCGATCAGCTGTCAACTCACTCAAGTTCCTCCAGATGTGCTGGAATG 430

DB 371 TGGCTGAAGCCGATCAGCTGTCAACTCACTCAAGTTCCTCCAGATGTGCTGGAATG 430

QY 431 CCCCATCAGAGACTTCTACTTCCAGAGTGTGACTAG 468

DB 431 CCCCATCAGAGACTTCTACTTCCAGAGTGTGACTAG 468

RESULT 9



LOCUS	1199 bp	mRNA	linear	HTC 03-APR-2000
DEFINITION	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210418104 product:interleukin 1 family, member 5 (delta), full insert sequence.			
ACCESSION	AK008977			
VERSION	AK008977.1 GI:12843490			
KEYWORDS	HTC, CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagasaki, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Teshiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
PUBMED	5			
REFERENCE	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
TITLE	Nature 420, 563-573 (2002)			
JOURNAL	6 (bases 1 to 1199)			
PUBMED	ADACHI, J., AIZAWA, K., AKAHIRA, S., AKIMURA, T., ARAI, A., ANO, H., ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FUKUNISHI, Y., FURUKO, M., HANAGAKI, T., HARA, A., HAYATSU, N., HIRAMOTO, K., HIRAKAWA, T., HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., IZAWA, M., KANUKAWA, T., KARI, H., KAWAI, J., KOJIMA, Y., KONO, H., KANDA, M., KOYA, S., KUTHARA, C., MATSUYAMA, T., MIYAZAKI, A., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OKAZAKI, Y., OKIDO, T., OWA, C., SAITO, H., SATO, R., SAKAI, C., SAKAI, K., SANO, H., SASAKI, D., SHIBATA, K., SHIBATA, Y., SHINAGAWA, A., SHIRAKI, T., SOGABE, Y., SUZUKI, H., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TANAKA, T., TEJIMA, Y., TOYA, T., YAMAMURA, T., YASUNISHI, A., YOSHIDA, K., YOSHINO, M., YURAMATSU, M. and HAYASHIZAKI, Y.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]			
TITLE	Please visit our web site (http://genome.gsc.riken.jp/) for further details.			
JOURNAL	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.			
COMMENT				

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'] GAGAGGAGAAGATCCAGAGCTCTTTTCTTTTTTTTAA 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGGAGAGATTCTCGAGTTAATTAAATTAAATCCCCCCCCC 3'). cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.

Host: SOLU.

```

Location/Qualifiers
1..1189
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:2210418104"
/db_xref="taxon:10090"
/clone="2210418104"
/sex="male"
/tissue_type="stomach"
/clone_1fb="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
130..600
/note="unnamed protein product: interleukin 1 family, member 5 (delta) (MGI:1859325)"
putative"
/codon_start=1
/protein_id="BAB26002.1"
/db_xref="GI:12843491"
/translation="MMVLSGLCFRMDALKVLINNNOLLAGSLHAEKYIKGEIRIVVPRADASIPVILGYQGSOCISCTEETGPPIKEPVIIMELYLAKSKSSTFFRRDMLTSSFSFAAYPGWFLCTSPBADPVRLTLPEDPADAPITDFPOOD"

```

ORIGIN

Query Match	Best Local Similarity	Matches
75.0%; Score 351.2; DB 4; Length 1189;	84.4%; Pred. No. 4.3e-86;	
Conservative 0; Mismatches 73; Indels 0; Gaps 0		
Db	1 ATGTCTCGAAGGGGCGCTGTGCTTCGGAATGAAGACTCGCAATTGAAGTGCTTAT	60
Db	133 ATGGTTTGAATGGGGCACTATAGCTTCGAATGAAGATTAAGCTTAGAAGTACGTAT	192
Qy	61 CTGCATAATAACAGCTCTTAGAGTGAAGGGCTGCATGAGAGGAAGTCAATTAAAGTGA	120
Db	193 CTGCACAATAACAGCTCTGCTGGTGAAGACTGCAACGAGAGAGTCAATTAAGGTAG	252
Qy	121 GAGATCAGCTGTGCCCATTCGGAGGTGAGTATGACAGCTGTCCCCTCATCTCGGAT	180
Db	253 GAGATCAGTGTGTCCCAAATCGGCACTGAGTGCAGTCTGTCCCTGTCAATCTTGAGC	312
Qy	181 GTCCAGGGTGAAGCCAATGCTGTCAATGTGGGGTGGGAGAGACCAGCTTAACACTA	240
Db	313 GTTCAAGGAGGAAGCAGTGCCTATCTTGTGGGACAGAGAAAGGCCAATTCTGAACCT	372
Qy	241 GAGCCAGTGAACATCATGAGACTCTATTTGGTGCAGAGAAATCAAGAGCTTCACTTC	300
Db	373 GAGCCAGTGAACATCATGAGACTCTACTCTCGGGGCAAGGAATCAAAAGAGCTTCACTTC	432
Qy	301 TACGGGGGGGACATGGGGCTCACCTCCAGCTTCAGATGGCTGCTACCGGGGCTGCTC	360
Db	433 TACGGGGGGGATATGGGCTTAACTTCCAGCTTCAGATCGCTGCTTACCCAGGCTGGTTC	492
Qy	361 CTGTGACAGGAGCTGGAAGCCGATCAGCTGTCAAGACTCAACCAAGCTTCCGAGAAATGAT	420
Db	493 CTTGCACTCAACCGGAAGCTGACCAAGCTGTCAAGGCTCACTCAAGATCCCTGAAGAACCC	552
Qy	421 GGCTGAATGCCCCCATCAAGACTTCTTCACTTCAGCAGTGTGACTAG	468
Db	553 GCCTGGAGTCTCCCATCAAGACTTCTTCACTTTCAGCAGTGTGACTAG	600

RESULT 11  
CBS90160 CBS90160

CBS90160 862 bp mRNA linear EST 03-APR-2003

DEFINITION AGENCOURT 12780806 NIH\_MGC\_136 Mus musculus cDNA clone  
IMAGE:30286859 5', mRNA sequence.  
ACCESSION CB590160  
VERSION CB590160.1 GI:29508016  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 862)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. David Rowe  
cDNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM321 row: m column: 12  
High quality sequence stop: 576.  
Location/Qualifiers  
1..862  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30286859"  
/tissue\_type="embryonic limb, maxilla and mandible"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_136"  
/note="Vector: pCMV-SPORT6.1; Site.1: EcoRV; Site.2: NotI;  
Normalized, full-length enriched library from pool of  
mouse embryonic limb, maxilla and mandible, embryonic day  
17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw  
equivalents from respective days). Cloned directionally,  
oligo-dT primed (5'-GACTAGTCTAGATGCGACGCGGCC(7)15-3'.  
Size selected for the >1kb fragments, average insert size  
1.2 kb. Normalization to Cot 7.5. Tissue contributed by  
David Rowe; library constructed by Resgen, Invitrogen  
Corp. Note: this is a NIH\_MGC library."

FEATURES  
source

ORIGIN

Query Match 74.7%; Score 349.6; DB 6; Length 862;  
Best Local Similarity 84.2%; Pred. No. 1.1e-85;  
Matches 394; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

1 ATGTCCTGAGTGGGGCGCTGCTTCCGAATGAAGAGCTGGCATTTAAAGTCTTAT 60  
85 ATGGTCTGAGTGGGGAATGATGCTTCCGAATGAAGAGATTCAGCCTTGAAAGTACTGAT 144  
61 CTGCATTAATTAACAGCTTTAGCTGAGGGCTGCATGACGAGAGGTCAATTAAGGTGA 120  
145 CTGCACATTAACAGCTGCTGCTGAGGACTGCACGACGAGAAGGTCAATTAAGGTGA 204  
121 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCCAGCTGTCCCGCTCATCTGGGT 180  
205 GAGATCAGTGTGTCCCAATCGGGGACTGATGCCAGTCTGTCCCTGTCACTCGGGC 264  
181 GTTCAGGGTGAAGCCAGTGGCTGTCTCATTTGGGGTGGGCGGACGACCTTAACACTA 240  
265 GTTCAAGGAGGAAGCCAGTGGCTATCTTGGGACAGAGAAAGGGCAATTTCTGAACCT 324  
241 GAGCCAGTAACATCATGAGCTCTATCTTGGTGCAGAGAAATCCAAAGCTTCACTTC 300  
325 GAGCCAGTAACATCATGAGCTCTATCTTGGGCGGACGAGAAATCCAAAGCTTCACTTC 384  
301 TACCGCGGGAGACATGGAGGCTCACTTCAGCTTGAAGTGGCTGAGTCCCGGGCTGGTTC 360  
385 TACCGCGGGAGATATGGGTCTTACTCTCACTTCGAATCGCTGCGCTCAACCAAGCTGGTTC 444

361 CTGTCACGAGTGGCTGTAAGCCGATAGCTGTGACACTCAACCACTTCCGAGAAATGT 420  
445 CTGTGACACTTCAACCGAAGCTGACAGCTGTCAAGGCTCACTTCAGATCTTGAAGACCCC 504  
421 GGCTGAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAG 468  
505 GCCTGGAGTGTCTCCATCAACAGACTTCTTCAAGCAGTGTGACTAG 552

RESULT 12  
CB589411  
LOCUS  
DEFINITION AGENCOURT 12770733 NIH\_MGC\_136 Mus musculus cDNA clone  
IMAGE:30286810 5', mRNA sequence.  
ACCESSION CB589411  
VERSION CB589411.1 GI:29507267  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 885)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. David Rowe  
cDNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM321 row: k column: 11  
High quality sequence stop: 241.  
Location/Qualifiers  
1..885  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30286810"  
/tissue\_type="embryonic limb, maxilla and mandible"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_136"  
/note="Vector: pCMV-SPORT6.1; Site.1: EcoRV; Site.2: NotI;  
Normalized, full-length enriched library from pool of  
mouse embryonic limb, maxilla and mandible, embryonic day  
17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw  
equivalents from respective days). Cloned directionally,  
oligo-dT primed (5'-GACTAGTCTAGATGCGACGCGGCC(7)15-3'.  
Size selected for the >1kb fragments, average insert size  
1.2 kb. Normalization to Cot 7.5. Tissue contributed by  
David Rowe; library constructed by Resgen, Invitrogen  
Corp. Note: this is a NIH\_MGC library."

FEATURES  
source

ORIGIN

Query Match 73.3%; Score 343.2; DB 6; Length 885;  
Best Local Similarity 83.3%; Pred. No. 6.6e-84;  
Matches 390; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

1 ATGTCCTGAGTGGGGCGCTGCTTCCGAATGAAGAGCTGGCATTTAAAGTCTTAT 60  
85 ATGGTCTGAGTGGGGAATGATGCTTCCGAATGAAGAGATTCAGCCTTGAAAGTACTGAT 144  
61 CTGCATTAATTAACAGCTTTAGCTGAGGGCTGCATGACGAGAGGTCAATTAAGGTGA 120  
145 CTGCACATTAACAGCTGCTGCTGAGGACTGCACGACGAGAAGGTCAATTAAGGTGA 204  
121 GAGATCAGCGTGTCCCAATCGGTGGCTGATGCCAGCTGTCCCGCTCATCTGGGT 180

Db	205	GAGATCAGTGTGTTGCCAAATCGGGCACAAGATTAACCACTGTGTCCCTGTCATCOTG96G	264
Qy	181	GTCCAGGGTGGAAAGCCATGCTGTCATGTGGGGTGGGGCAGAGGCCACTCTTAACACTA	240
Db	265	GTTCAAGAGAGAAAGCCAGTGGCTTACTTGTGGGACAGGAAAGGGCCAAATCTGAAACTT	324
Qy	241	GAGCCAGTGAACATCATGTAGAGCTCATCTTGTGGTGCCAAGAAATCCAAAGCTTCAACCTTC	300
Db	325	GAGCCAGTGAACATCATGTAGAGCTCTTACTTCGGGGCCAAAGAAATCAAAAGCTTCACTTC	384
Qy	301	TACCGGGCGGACATGGGGCTCACTCCAGCTTCAGTCCGCTGCTTACCCGGGCTGTTC	360
Db	385	TACCGGGCGGATATAGGTCTTAACCTCCAGCTTCGAAATCCGGTCTTACCCAGGGCTGTTCC	444
Qy	361	CTGTGACACGTGGCTCTGAAGCCGATGACCTGTCAAGCTCACCCAGCTTCCGAGAGTGT	420
Db	445	CTGTGACACTCAACCCGAAAGCTGACCCAGCTGTCAAGCTCATCTGAGAGGAGACCC	504
Qy	421	GGCTGGATGGCCCCCATCAAGACTTCACTTCCAGCAGTGGACTAG	468
Db	505	GCTGGAGTGTCTCCATCAAGACTTCACTTCCAGCAGTGGACTAG	552
RESULT 13			
AK014576			
LOCUS	AK014576	2841 bp	mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632413M13 product:interleukin 1 family, member 5 (delta), full insert sequence.		
ACCESSION	AK014576		
VERSION	AK014576.2	GI:26105970	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ilegami, T., Kashiwagi, K., Fujisake, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipipillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	11076861		
REFERENCE			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
PUBMED	5		
REFERENCE			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
PUBMED	6 (bases 1 to 2841)		

**AUTHORS**  
 Aachichi,T., Aizawa,K., Akhira,S., Akimura,T., Arii,A., Aono,H.,  
 Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,  
 Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hizumoto,K.,  
 Hirakawa,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,  
 Kasekawa,T., Kato,H., Kawai,J., Kojima,Y., Komuro,H., Kouda,M.,  
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,Y., Nihi,K.,  
 Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,  
 Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D.,  
 Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y.,  
 Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,  
 Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,  
 Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
**TITLE**  
 Direct Submission  
**JOURNAL**  
 Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gs.c.riken.jp,  
 URL:http://genome.gs.c.riken.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
**COMMENT**  
 On Dec 6, 2002 this sequence version replaced gi:12852516.  
 Please visit our web site (http://genome.gs.c.riken.jp/) for further  
 details.  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues. First strand cDNA was primed with a primer  
 [5' GAGAGAGAGAGATCCCAAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse transcriptase  
 and subsequently enriched for full-length by cap-trapper. cDNA went  
 through one round of normalization to Rot = 10.0 and subtraction to  
 Rot = 100.0. Second strand cDNA was prepared with the primer  
 adapter of sequence [5'  
 GAGAGAGAGATCTCGAGTTAATTAAATTAATCCCCCCCC 3']. cDNA was cleaved  
 with BamHI and XhoI. cDNA of size compressed longer than 7 kb was  
 selected before cloning. Vector: a modified plasmid pUC19 after  
 bulk excision from Lambda PLC 1. Cloning sites, 5' end: SalI, 3'  
 end: BamHI. Host: DH10B.  
**FEATURES**  
 source  
 location/Qualifiers  
 1..2841  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="FANTOM:DB:4632413N13"  
 /db\_xref="taxon:10090"  
 /clone\_id="4632413N13"  
 /tissue\_type="skin"  
 /clone\_lib="RIKEN full-length enriched mouse cDNA library"  
 /dev\_stage="0 day neonate"  
 318..787  
 /note="interleukin 1 family, member 5 (delta)  
 (MGI:1859325)  
 putative"  
**ORIGIN**  
 Query Match 72.8%; Score 340.8; DB 4; Length 2841;  
 Best Local Similarity 84.4%; Pred. No. 3,9e-83;  
 Matches 395; Conservative 0; Mismatches 72; Indels 1; Gaps 1;  
**QY** 1 ATGTCCTGAGTGAGGGCGCTGCTCTCCGATGAAGAGACTCGGCATTAAGTGCTTTAT 60  
**Db** 321 ATGGTTCTGATGGGGACATATGCTTCCGATGAAGAGATTCACTTTGAAGTACTGTAT 380  
**QY** 61 CTGCATTAATACAGAGCTTCTAGCTGAGGGCTGTCAGGAGGAGGAAGCTAATAAGGGA 120  
**Db** 381 CTGCACATTAACAGAGCTGCTGCTGAGAGACTGACACGACAGAAAGTCATTAAGGAG 440  
**QY** 121 GAATATCAGCGTGTCCCAATCGGTGGCTGATGCCAGCGCTGCCCCGTCATCTGGGT 180  
**Db** 441 GAATATCAGTGTTCCTCCAAATCGGGACCTGGAATGCCAGTGTGCTCCCTGTCACTCGGG 500  
**QY** 181 GTCCAGGGTGAAGCAAGTGCCTGTCTATGTGGGTGGGGCGAGAGCCGACTTAACCTA 240



[illegible]

	72.3%;	Score 338.4;	DB 5;	Length 708;	
Query Match	Best Local Similarity	82.7%;	Pred. No. 1.4e-82;		
Matches	387;	Conservative	0; Mismatches	81; Indels	0; Gaps
 ORIGIN					
1	ATGGTCCTGAGTGGCGGCTGTGCTTCGCCAATGAAGAAGCATTCGGCATTGAAGTGCTTTAT	60			
223	ATGGTTCAGTAGTGGGGCACTATGCTCCGAAATGAAGGATTAACGCCTTGAAAGTACTGAT	292			
61	CTGCATAATAACAAGCTTCTAGCTGGAGGGGCTGCATGAGGGAAGGTCATTAAAGGTAA	120			
293	CTGCACATAAACAGCTGCTGCTGGAGAGACTGCAACGAGGAAGAGTATTAAAGGTGAG	352			
121	GAGATCAGCGTGTGTCCCCAATCGGTGGGTGATGCCAGCCTGTCCCCTGATCTGTGGT	180			
Db	333 GAGATCAGTGTGTGTCCCAAATCGGGCACTGGAATGCACTGTGTCCCTGTATCTGTGGC	412			
Qy	181 GTCCAGGGTGAAGCCAGTGCCTGTGATGTGGGGGTGGGACAGAGCCGCACTCTAACTA	240			
Qy	413 GTTCAAGAGAAAGCCAGTGCCTATCTGTGGGACAGAAAGGGCCAAATCTGAAACTT	472			



DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Homo sapiens (human)					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Homo sapiens					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				1 (bases 1 to 414)					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Ebert, L., Hell, O., Hennig, S., Korn, B., Neubert, P., Partsch, E., Peters, M., Radelof, U. and Schneider, D.					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				I.M.A.G.E. cDNA Clone Collection					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Unpublished (2004)					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Contact: Inge Axlart					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Heubnerweg 6, D-14059 Berlin, Germany					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Email: www.rzpd.de					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				RZPD; IMAGp98M234181.					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				RZPDLIB; I.M.A.G.E. cDNA Clone Collection;					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Contact: Inge Axlart					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Heubnerweg 6, D-14059 Berlin, Germany					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Tel: +49 30 32639 100					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Fax: +49 30 32639 111					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				www.rzpd.de					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				This clone is available royalty-free from RZPD.					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Contact RZPD (clone: rzd4) for further information. Seq primer:					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				M13u, Primer sequence: CGTGTGTAACGACGGCCAGT.					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				Location/Qualifiers					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				1. .414					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				/organism="Homo sapiens"					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				/mol_type="mRNA"					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				/db_xref="taxon:9606"					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				/clone="IMAGp98M234181 ; IMAGE:1647934"					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				/tissue_type="parathyroid tumor"					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				/dev_stage="adult"					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				/lab_host="DH10B (ampicillin resistant)"					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272				/clone_1lb="Soares parathyroid tumor NbHRA"					
Oy	CR742272	414 bp mRNA linear EST 21-DEC-2004	CR742272									

ORIGIN	NIH."
Query Match	72.2%; Score 338; DB 7; Length 414;
Best Local Similarity	99.1%; Pred. No. 1.6e-82;
Matches 349; Conservative	0; Mismatches 2; Indels 1; Gaps 1;
Qy	1 ATGTCCTGAGTGGGGCGCTGTGCTCCGATGAAAGACCTCGCATTTGAAGGTGCTTTAT 60
Db	63 ATGGTCCTGAGTGGGGCGCTGTGCTTCGATGAAAGACCTCGCATTTGAAGGTGCTTTAT 122
Qy	61 CTGATATATATACCAAGCTTTAGCTGGAAGGGGTGATGAGGGAAGGTCAATTAAGTAA 120
Db	123 CTGATATATATACCAAGCTTTAGCTGGAAGGGGTGATGAGGGAAGGTCAATTAAGTAA 182
Qy	121 GAGATCAAGCGTGTCCTCCCAATCGGTGAGTGGATCCAGCCTGTCCCGGTATCCTGGGT 180
Db	183 GAGATCAAGCGTGTCCTCCCAATCGGTGAGTGGATCCAGCCTGTCCCGGTATCCTGGGT 242
Qy	181 GTCCAGGGGTGAAACCAGTGTCTTCAATGTGGGGTGGGGCAGAGCCGACTCTAACA 240
Db	243 GTCCAGGGGTGAAACCAGTGTCTTCAATGTGGGGTGGGGCAGAGCCGACTCTAACA 302
Qy	241 GAGCCAGTGAACATCATGAGAGCTCTATCTTGTGTGCCAAGATCCAAAGAGCTTCAACCTTC 300
Db	303 GAGCCAGTGAACATCATGAGAGCTCTATCTTGTGTGCCAAGATCCAAAGAGCTTCAACCTTC 362
Qy	301 TACGGGGGGGACATGAGGGCTCACTCCAG-CTTGAGATCGGTGCTTAACCCG 351
Db	363 TACGGGGGGGACATGAGGCTCACTCCAGCTTGAAGTGGCTGCTTAACCCG 414

RESULT 16	
AKO10020	
LOCUS	AKO10020 1531 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:231063B08 product:interleukin 1 family, member 5 (delta), full insert sequence.
ACCESSION	AKO10020
VERSION	AKO10020.1 GI:12845175
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCES	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishire, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kasaiwaqi, K., Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6 (bases 1 to 1531)  
AUTHORS Adachi, J., Alizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kikukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Tanabe, T., Tanaka, T., Tejima, Y., Toya, T., Yamamuro, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
TITLE Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: //genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.  
FEATURES  
source  
1..1531  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="PANTOM DB:2310063B08"  
/db\_xref="taxon:10090"  
/clone="2310063B08"  
/sex="male"  
/cisse\_type="tongue"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="adult"  
228..694  
/note="Interleukin 1 family, member 5 (delta)"  
misc\_feature  
1000..1531  
/note="putative"  
ORIGIN  
Query Match 71.2%; Score 333.2; DB 4; Length 1531;  
Best Local Similarity 83.5%; Pred. No. 4,4e-81;  
Matches 391; Conservative 0; Mismatches 73; Indels 4; Gaps 1;  
QY 1 ATGGTCTGAGTGGGCGCTGTCTCCGATGAAAGGACTCGGATTTGAAGTCTTTAT 60  
DB 231 ATGGTCTGAGTGGGCGCTGTCTCCGATGAAAGGACTCGGATTTGAAGTCTTTAT 290  
QY 61 CTGCATTAATTAACGAGCTTTAGCTGAGGCGCTGATGAGGAGGAGGATTTAAAGGTGA 120  
DB 291 CTGCATTAATTAACGAGCTTTAGCTGAGGCGCTGATGAGGAGGAGGATTTAAAGGTGA 350

QY 121 GAGATCAGCGTGTGCTCCCAATCGGTGAGTATCCAGCTGTGCTCCCGATCTTGGGT 180  
DB 351 GAGATCAGTGTGTGCTCCCAATCGGTGAGTATCCAGCTGTGCTCCCGATCTTGGGT 410  
QY 181 GTCCAGGCTGAGGAGCCAGCTGCTGTATGTTGGGTCAGAGAGCCAGCTTAACTA 240  
DB 411 GTTCAGAGGAGGAGCCAGCTGCTGTATGTTGGGTCAGAGAGGAGCCAGCTTAACTA 470  
QY 241 GAGCCAGGAGCATCATGAGGAGCTGTATGTTGGGTCAGAGAGGAGGAGCTTCACTTC 300  
DB 471 G---AGTGAACATCATGAGGAGCTGTATGTTGGGTCAGAGAGGAGGAGCTTCACTTC 526  
QY 301 TACCGGCGGAGCATGAGGAGCTGTATGTTGGGTCAGAGAGGAGGAGCTTCACTTC 360  
DB 527 TACCGGCGGAGCATGAGGAGCTGTATGTTGGGTCAGAGAGGAGGAGCTTCACTTC 586  
QY 361 CTGTCACGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
DB 587 CTGTCACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 646  
QY 421 GCTGAGATGCTCCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 468  
DB 647 GCTGAGATGCTCCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 694

RESULT 17  
AY413264 439 bp DNA linear GSS 17-DEC-2003  
LOCUS AY413264  
DEFINITION Mus musculus IL1F5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
ACCESSION AY413264  
VERSION AY413264.1 GI:39769226  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.  
1 (bases 1 to 439)  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 439)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source  
1..439  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/gene="IL1F5"  
/locus\_tag="HMC4832"

ORIGIN  
Query Match 69.9%; Score 327; DB 10; Length 439;  
Best Local Similarity 84.1%; Pred. No. 1.8e-79;  
Matches 369; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
QY 30 AATGAGAGCTGCGCATTAAGGCTTTATCTGCTAATTAACGAGCTTTAGCTGAGG 89

Db 1 AATGAGATTCAGCTTGAGGTAAGTACTGATCTGACAAATAACAGACTGCTGGCTGAGG 60  
 QY 90 GGTGCAATGAGGAGGAGTATTAAGTAAAGATCAGCTGCTGCTCCATGCTGCT 149  
 Db 61 ACTGACGAGAGAGAGTATTAAGTAAAGATCAGCTGCTGCTCCATGCTGCT 120  
 QY 150 GGATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209  
 Db 121 GGATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 QY 210 TGGGCTGAGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269  
 Db 181 TGGGAGAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 QY 270 TGGTGCAGAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329  
 Db 241 CGGGGAGAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 QY 330 CTTCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389  
 Db 301 CTTCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 390 TGTGAGACTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449  
 Db 361 TGTGAGACTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 QY 450 CTTCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468  
 Db 421 CTTCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439

RESULT 18  
 LOCUS BX477358 338 bp mRNA linear EST 04-SEP-2003  
 DEFINITION DKFZp686022193\_r1 686 (synonym: h1cc3) Homo sapiens cDNA clone  
 ACCESSION BX477358  
 VERSION BX477358.1 GI:31674556  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 338)  
 AUTHORS Anseorge, W., Krieger, S., Regiert, T., Rittmüller, C., Schwager, B.,  
 Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and  
 Wiemann, S.  
 TITLE EST (Anseorge, W., Krieger, S., Regiert, T., Rittmüller, C., et al.)  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: MIPS  
 MIPs  
 Ingelstaedter Landstr. 1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
 sequenced by EMBL (European Molecular Biology Laboratories,  
 Heidelberg/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No 81 sequence available.  
 This clone (DKFZp686022193) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
 Location/Qualifiers  
 source  
 1. 338  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKFZp686022193"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_1ib="686 (synonym: h1cc3)"  
 /note="Vector: pTribex2; site\_1: sf1a; site\_2: sf1b;

ORIGIN  
 cdna-collection"  
 Query Match 57.9%; Score 271; DB 5; Length 338;  
 Best Local Similarity 100.0%; Pred. No. 5, 6e-64;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGGCTCTAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
 Db 68 ATGGCTCTAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127  
 QY 61 CTGCATATATACAGCTTCTAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 128 CTGCATATATACAGCTTCTAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187  
 QY 121 GAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 Db 188 GAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247  
 QY 181 GTTCAAGGAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 Db 248 GTTCAAGGAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307  
 QY 241 GAGCAGTGAACATCATGAGGCTCTATCTT 271  
 Db 308 GAGCAGTGAACATCATGAGGCTCTATCTT 338

RESULT 19  
 LOCUS CB194288 898 bp mRNA linear EST 05-FEB-2003  
 DEFINITION AGENCOURT\_11259798 NIH MGC\_135 Mus musculus cDNA clone  
 ACCESSION CB194288  
 VERSION CB194288.1 GI:28218671  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 898)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE NIH-MGC  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: Dr. David Rowe  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDAM0034 row: a column: 08  
 High quality sequence start: 16  
 High quality sequence stop: 652.  
 Location/Qualifiers  
 source  
 1. 898  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:30135655"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1ib="NIH MGC 135"  
 /note="Vector: pCMVSPORT6.1; Site 1: BcoRV; Site 2: NotI;  
 Normalized full-length enriched library from pooled mouse  
 embryonic limb, maxilla and mandible, day 12.5, 13.5,  
 14.5, and 15.5 (size selected for the 0.5-1 kb fragments)  
 cloned directionally, priming method: Oligo-dT. cDNA  
 enrichment: >1k bp, Average insert size 1.6k bp.  
 Normalization (Cot value): 7.5 kb. Priming sequence:  
 5'-GACTAGTCTAGATCCGAGCGCCGCCCT(T)3' Tissue contributed



Oy 128 GGGTGGTCCCAATGGGTGGCTGGAAATGCCAGCTGGCCCCCGCATCTCTGGGGTGTCCAG 187  
 Db 1 GTGTGTGCCAATGGGGCACTGGAGTGCAGTGTGCCCTGTCACTCTGGGGGTCCAAG 60  
 Oy 188 GTGGAAGCCAGTGGCTGTCACTGTGGGGTGGGGCAGGAGCCGACTTAACTAAGACCAG 247  
 Db 61 GAGGAAGCCAGTGGCTATCTTGTGGGACAGAGAAAGGCCAATTCTGAAACTTGAAGCCAG 120  
 Oy 248 TGAACATCATGGAGCTCTATCTTGGTGCCAGGAATCCAAGACTTCACCTTCTACCGGC 307  
 Db 121 TGAACATCATGGAGCTCTACCTCGGGGCCAAGGAATCAAGAAGCTTCACCTTCTACCGGC 180  
 Oy 308 GGGACATGGGGCTCACCTTCAGCTTGAAGTCGGCTGCTTACCOCGGCTGGTTCCTGTGCA 367  
 Db 181 GGGATATGGGTCTTACCTTCACCTTCGAATTCGGCTGCTTACCAGGCTGGTTCCTGTGCA 240  
 Oy 368 CGGTGCTCGAAGCCCATCAGCTGTGCAGACTACCCAGCTTCCGAGGAATGGTGGCTGGA 427  
 Db 241 CCTCACCGGAAGCTGACGAGCTGTCAAGGCTCACTCAAGTCCCTGAGGAGACCCCGCTGGG 300  
 Oy 428 ATGCCCCCATCAGAGACTTCTACTTCCACAGTGTGACTTAA 468  
 Db 301 ATGCTCCCATCAGAGCTTCTACTTTCACAGAGTGTGACTTAA 341

RESULT 21	BY708859	LOCUS	BY708859	666 bp	mRNA	linear	EST 16-DEC-2007
DEFINITION	BY708859	RIKEN full-length enriched, adult male stomach Mus musculus cDNA Z110418104 5', mRNA sequence.					
ACCESSION	BY708859						
VERSION	BY708859.1	GI:27120053					

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Scuriognathi; Muroidae; Muridae; Murinae; Mus.

## REFERENCE AUTHORS

**TITLE** Analysis of the mouse transcriptome based on functional annotation

JOURNAL  
PUBMED

**COMMENT**

Laboratory for Genome Exploration Research Group, RIKEN Genomic

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel.: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
 Email: [genomeres@sc.riken.jp](mailto:genomeres@sc.riken.jp), URL: <http://genome.gsc.riken.jp/>  
 Aizuchi, Y., Aizawa, K., Akimura, T., Arkawa, T., Carninci, P.,  
 Fukuda, S., Hashizume, W., Hayashida, K., Hirose, T., Hori, F.,  
 Imotani, K., Ishii, Y., Itoh, M., Kageawa, H., Kawai, J., Koima, Y.,  
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
 Nomura, K., Numazaki, R., Ono, M., Oshio, K., Shiraki, T., Sakazume, N.,  
 Sano, H., Saeki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,  
 Takeda, Y., Waki, K., Watanuki, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome*. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

```

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2210418104"
/sex="male"
/tissue_type="stomach"
/dev_stage="adult"
/lab_host="SOLR"
/clone_1ib="RIKEN full-length enriched, adult male
stomach"
/note="Site 1: XhoI; Site 2: SctI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGGAGGAGGCGCGCGCACTCGAGCTTTTTTTTTTTTTVN 3'}. cDNA was
prepared by using trihalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence 15'
GAGGAGGAGATTTCGAGTAAATTAATTAATTCCTCCCCCCCC 3'}. cDNA
was cleaved with XhoI and SctI."

```

ORIGIN

Query Match	51.0%;	Score 238.8;	DB 5;	Length 686;
-------------	--------	--------------	-------	-------------

Matches 299; Conservative 0; Mismatches 62; Indels 3; Gaps 2

1 ATGCTCCTGAGTGGGCGCTGTCTTCCGAATGAAGACTCGGCATTGAAGGTCTTAT 60

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

.....

[illegible]

121 GAGATCAGCGTGGTCCCAATCGGTGGCTGGATGCGAGCCCTGTCCCTCCCTCATCCCTGGGT 180

Db	253	GAGATCAATGTGTTGTCCTCCAAATCGGCACTGGATGCCAATCTGTGTCCTCTGTCATCTTGGGC	312
Qy	181	GTCCAGGCTGGAAAGCCAGTGCCTGTTCATATGTGGGCTGGGCGAGAGCCGACTTAACACTA	240
Db	313	GTTCAAGAGGAGGAGCCAGTGCCTATCTTGTGGGACAGAGAAAGGCGCAATCTGAACCTT	372
Qy	241	GAGCCAGTGAACATATGAGAGCTCTATCTTGTGGTCCAAAGAAATCCAGAGCTTACCTTC	300
Db	373	GAGCCAGTGAACATATGAGAGCTCTACTCTCGGGGCGCCAAAGATCAAAGAGCTTACCTTT	432
Qy	301	TACCGGCGGGGACATCGGGGCTCCTCTCCAGCTT--CGAGTGGGCTGCCTACCCCGGGCTGG	357
Db	433	TTCCGGCGGAGATATGGTGCTTACTTCCAGCTTTTGAATCCGGTTGCTACCCCGAGCTGG	492
Qy	358	TTCC 361	
Db	493	TTTC 496	
RESULT 22	W08205		
LOCUS	W08205	382 bp mRNA linear EST 05-SEP-1996	
DEFINITION	mb49b1.r1 Soares mouse p3MMPf9.5 Mus musculus cDNA clone		
ACCESSION	IMAGE:332733 5' similar to PIR:A49031 A49031 interleukin 1 receptor		
VERSION	W08205		
KEYWORDS	antagonist - mouse ; mRNA sequence.		
SOURCE	W08205.1 GI:1282415		
ORGANISM	EST.		
REFERENCE	Mus musculus (house mouse)		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Schizognathini; Muridae; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 382)		
JOURNAL	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.		
COMMENT	The WashU-HM Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HM Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LINT ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:214133 Seq primer: EMP1 primer High quality sequence stop: 354.		
FEATURES	Location/Qualifiers		
source	1..382		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:332733"		
	/dev_stage="19.5 dpc total fetus"		
	/lab_host="PH10B (ampicillin resistant)"		
	/clone_1lb="Soares mouse p3MMPf9.5"		
	/note="Vector: p773D (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15', TCTTCCCATCTGAAGTGGAGCGGCGCGCATTTTCTTTTCTTTT 3'1, double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by		

ORIGIN	Dr. Minoru Ko (Wayne State University)."
Query Match	44.6%, Score 208.6; DB 8; Length 382;
Best Local Similarity	84.2%; Pred. No. 1,1e-46;
Matches 235; Conservative	0; Mismatches 44; Indels 0; Gaps 0;
QY	1 ATGGCTCCAGATGGGGGCGCTGTGCTTCGGAATGAAGACCTCGCATTTGAAGGCTTTAT 60
DB	104 ATGGCTTCGAATGGGGCACTATGCTTCGGAATGAAGATTCAGCTTGAAGGTACTGTAT 163
QY	61 CTGCATAATACCAAGCTTCTAGCTGAGAGGCGCTGATCGAGGAAGTCAATTAAGGTGAA 120
DB	164 CTGCACATTAACAGCTCTGCTGCTGAGAGATGACACCGAAGAAAGTCAATTAAGGTGAG 223
QY	121 GAGATCAGCGTGTGCTCCCAATCGGTGGGTGATGCCAGCTGTCTCCCGCTCATCTGGGT 180
DB	224 GAGATCAAGTGTGTGCTCCCAATCGGGCACTGATGCCAGTGTGTCTCCCTGTCATCTGGGC 283
QY	181 GTCCAGGTTGAGAACCGCATGTGCTGTCAATGTGGGTGGGGCAGAGCCGACTCTAACACTA 240
DB	284 GTTCAGGAGGAGAGCAAGTGTCTATCTTGTGGGACAGAGAAAGGCCCAATTCGAACTT 343
QY	241 GAGCCAGTGAACATCATGATGAGCTCTATCTTGTGTGCCAAG 279
DB	344 GAGCCAGTGAACATCATGATGAGCTCTTACTCGGGGCCAAG 382
RESULT 23	
LOCUS	BY109350 348 bp mRNA linear EST 07-DEC-2002
DEFINITION	BY109350 RIKEN full-length enriched, 15 days embryo whole body Mus musculus CDNA clone L330027E19.5, mRNA sequence.
ACCESSION	BY109350
VERSION	BY109350.1 GI:26219967
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Mus.
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanka, I., Kiyosawa, H., Yagi, K., Tomaru, I., Hasegawa, I., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schirral, L. M., Kanapin, A., Matsuda, H., Barilov, S., Beisel, K. W., Blake, J. A., Brzde, D., Bursic, V., Fletcher, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frizer, K. S., Gaasterland, T., Gariboldi, M., Gassi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, P. A., Konagaya, A., Kurochkin, I. V., Lee, Y., Lemhard, B., Lyons, P. A., Maglott, D. R., Malraiz, L., Marchionni, L., McKenzie, L., Mikti, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravech, J. C., Reed, J. C., Reed, J. C., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Waranabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavoian, M., Zhu, Y., Zimmer, A., Carrinck, P., Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ichii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE	Analysis of the mouse transcriptome based on functional annotation
JOURNAL	Nature 420, 563-573 (2002)
PUBMED	12466851

## COMMENT

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,  
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
 Shiraki, T., Tagami, M., Waki, K., Watanahiki, A., Muramatsu, M. and  
 Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.

## FEATURES

source

Location/Qualifiers  
 1. 348  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U330027E19"  
 /tissue\_type="whole body"  
 /dev\_stage="15 days embryo"  
 /clone\_1b="RIKEN full-length enriched, 15 days embryo  
 whole body"

## ORIGIN

Query Match 35.6%; Score 166.6; DB 5; Length 348;  
 Best Local Similarity 86.4%; Pred. No. 4.8e-35;  
 Matches 184; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

1 ATGGTCCTGAGTGGGCGCTGCTCCGAATGAAGAGACTCGGCAATTAAGGCTTTAT 60  
 Db ATGGTCCTGAGTGGGCGCTGCTCCGAATGAAGAGACTCGGCAATTAAGGCTTTAT 195  
 61 CTGCATTAATTAACAGCTTCTAGCTGAGAGGCTGCATGACAGGAGGCTTAAGGTGA 120  
 Db CTGCACAAATTAACAGCTTCTAGCTGAGAGGCTGCATGACAGGAGGCTTAAGGTGA 255  
 121 GAGATCAGCGTGTCTCCCAATGCTGCTGATGCCAGCTGTCCCTCATCTGGGT 180  
 Db GAGATCAGCGTGTCTCCCAATGCTGCTGATGCCAGCTGTCCCTCATCTGGGT 315  
 256 GAGATCAGCGTGTCTCCCAATGCTGCTGATGCCAGCTGTCCCTCATCTGGGT 315  
 181 GTCCAGGGTGAAGCAGGCTGCTCATGTGGG 213  
 Db GTCCAGGGTGAAGCAGGCTGCTCATGTGGG 348

RESULT 24  
 BY107750 343 bp mRNA linear EST 07-DEC-2002  
 LOCUS BY107750 RIKEN full-length enriched, 15 days embryo whole body Mus  
 DEFINITION Musculus cDNA clone U330014H07 5', mRNA sequence.  
 ACCESSION BY107750  
 VERSION BY107750.1 GI:26218367

## KEYWORDS

## SOURCE

EST.  
 Mus musculus (house mouse)  
 Mus musculus

## ORGANISM

Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia;  
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Nikaido, I., Ogaso, N., Saito, R., Suzuki, H., Yamataka, I.,  
 Kiyonaka, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schönbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bull, C.,  
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapf, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brucic, V.,  
 Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dargatz, T.A.,  
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
 Numata, K., Okido, T., Pavan, W.J., Pereira, G., Pesole, G.,  
 Petrovsky, N., Pillai, R., Pontius, D.U., Qi, D., Ramachandran, S.,  
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
 Wells, C., Wilming, L.G., Wyshew-Boris, A., Yanagisawa, M., Yang, I.,  
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
 Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,  
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
 Arakawa, T., Fukuda, S., Hara, A., Hashitume, M., Imotani, K., Ishii, Y.,  
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
 Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 1246851

## JOURNAL

CONTACT: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216

## COMMENT

FEATURES  
 source

Location/Qualifiers  
 1. 343  
 /organism="Mus musculus"



```
/mol_type="mRNA"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="L330014H07"  
/issue_type="whole body"  
/dev_stage="15 days embryo"  
/clone_lib="RIKEN full-length enriched, 15 days embryo  
whole body"
```

## ORIGIN

```
Query Match      34.5%; Score 161.6; DB 5; Length 343;  
Best Local Similarity 86.1%; Pred. No. 1.2e-33;  
Matches 179; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
```

```
OY 1 ATGTCCTGAGTGGGCGCTGCTGCTTCCGAATGAAGGACTCGGCATTGAAGTCTTAT 60  
DB 136 ATGTCCTGAGTGGGCGCTGCTGCTTCCGAATGAAGGACTCGGCATTGAAGTCTTAT 195  
OY 61 CTGCATATTAACACGCTTCTAGCTGAGAGGGCTGCATGCAGAGGAGTCAATTAAGTGA 120  
DB 196 CTGCATATTAACACGCTTCTAGCTGAGAGGGCTGCATGCAGAGGAGTCAATTAAGTGA 255  
OY 121 GAGATCAGCGTGTGTCCTCCCATCGCTGCTGATGCACGCTGTCCCGCTCATCTGGGT 180  
DB 256 GAGATCAGGTGTGTCCCAATATGGGACATGCAGTCTGTCCCGCTCATCTGGGC 315  
OY 181 GTCCAGGGTGAAGCCAGTGCCTGTCTAT 208  
DB 316 GTTCAAGGAGGAAGCCAGTGCCTATCTT 343
```

```
RESULT 25  
CK947864      689 bp      mRNA      linear      EST 15-MAR-2004  
LOCUS      4072568 BARC 10BOV Bos taurus cDNA clone 10BOV23_A09 5', mRNA  
DEFINITION      sequence.  
ACCESSION      CK947864  
VERSION      CK947864.1 GI:45462244  
KEYWORDS      EST.  
SOURCE      Bos taurus (cow)  
ORGANISM      Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 689)
```

```
REFERENCE  
AUTHORS      Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,  
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.  
TITLE      Production of EST from cDNA libraries derived from immunologically  
activated bovine gut  
JOURNAL  
COMMENT      Unpublished (2004)  
CONTACT: Tad S. Sonstegard  
Bovine Functional Genomics Laboratory  
Animal and Natural Resources Institute  
Bldg. 200 Rm2a BARC-East, Beltsville, MD 20705, USA  
Tel: 3015048416  
Fax: 3015048414  
Email: tade@anri.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
0.000925 using options -trim alt "-trim fasta. Vector identified  
by cross match using options -mismatch 12 -minscore 12  
Plate: 23 row: A column: 09  
Seq primer: CCCAGTCACGACCTGTGAACG  
High quality sequence stop: 689.  
Location/Qualifiers
```

```
FEATURES  
source  
1..689  
/organism="Bos taurus"  
/mol_type="mRNA"  
/strain="Holstein"  
/db_xref="taxon:9913"  
/clone="10BOV23_A09"  
/sex="Male"  
/issue_type="Pooled"  
/dev_stage="Multiple"
```

```
/lab host="DH10B T1 phage resistant"  
/clone_lib="BARC 10BOV"  
/note="Organ: Small Intestine; Vector: pagen-1; Site 1:  
EcorV; Site 2: NotI; Equimolar amounts of mRNA extracted  
from proximal jejunums of 18 and 21 wk old steers, and  
distal ileums of 14 day old calves. proximal jejunum  
exposed to C. oncophora for 3 and 6 weeks, and distal  
ileum exposed to C. parvum for 7 days"
```

## ORIGIN

```
Query Match      34.2%; Score 160; DB 7; Length 689;  
Best Local Similarity 76.6%; Pred. No. 3.7e-33;  
Matches 196; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
```

```
OY 213 GTGGGGAGAGAGCGGACTTAACTAGAGCCAGTGAACATCATGAGCTTATCTTGG 272  
DB 172 GAGGCGCTTAAAGGGGAGAGTCAATTAAGCCAGTGAACATCATGAGCTTACACAG 231  
OY 273 TGCCAGGATTCAGAGCTTACACTTCTACCGCGGACATGGGCTTACCTCCAGCTT 332  
DB 232 TGCCAGGAGTCTAAAAATTCACTTCTACCGCGGACACGGGGCTCACCTCCAGCTT 291  
OY 333 CGAGTCGCTGCTTACCGGCTGTCTCTGTGACAGGTGCTGAAGCCGATCAGCTGT 392  
DB 292 TGAGTCGGCTGCTTACCGGCTGTCTCTGTGACAGGTGCTGAAGCCGATCAGCTCT 351  
OY 393 CAGATCCACGACTTCCCGAATGTGGTGGAAATCCCGCATCAGACTTACTT 452  
DB 352 GCAGATCCACGACTTCCCGAAGGACACGAGTGGACAAACCATCATGACTTACTT 411  
OY 453 CCAGCAGTGTACTAG 468  
DB 412 CCAGCATGTGACTAG 427
```

```
RESULT 26  
CK952430      702 bp      mRNA      linear      EST 15-MAR-2004  
LOCUS      4091856 BARC 10BOV Bos taurus cDNA clone 10BOV29_L23 5', mRNA  
DEFINITION      sequence.  
ACCESSION      CK952430  
VERSION      CK952430.1 GI:45466810  
KEYWORDS      EST.  
SOURCE      Bos taurus (cow)  
ORGANISM      Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 702)
```

```
REFERENCE  
AUTHORS      Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,  
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.  
TITLE      Production of EST from cDNA libraries derived from immunologically  
activated bovine gut  
JOURNAL  
COMMENT      Unpublished (2004)  
CONTACT: Tad S. Sonstegard  
Bovine Functional Genomics Laboratory  
Animal and Natural Resources Institute  
Bldg. 200 Rm2a BARC-East, Beltsville, MD 20705, USA  
Tel: 3015048416  
Fax: 3015048414  
Email: tade@anri.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
0.000925 using options -trim alt "-trim fasta. Vector identified  
by cross match using options -mismatch 12 -minscore 18  
Plate: 29 row: L column: 23  
Seq primer: CCCAGTCACGACCTGTGAACG  
High quality sequence stop: 702.  
Location/Qualifiers
```

```
FEATURES  
source  
1..702  
/organism="Bos taurus"  
/mol_type="mRNA"  
/strain="Holstein"  
/db_xref="taxon:9913"
```



/clone="10BOV29\_L23"  
/sex="Male"  
/tissue\_type="Pooled"  
/dev\_stage="Multiple"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="BARC 10BOV"  
/note="Organ: Small intestine; Vector: pagen-1; Site 1: EcorV; Site 2: NotI; Equimolar amounts of mRNA extracted from proximal jejunum of 18 and 21 wk old steers, and distal ileum of 14 day old calves. proximal jejunum exposed to C. oncophora for 3 and 6 weeks, and distal ileum exposed to C. parvum for 7 days"

## ORIGIN

Query Match 34.2%; Score 160; DB 7; Length 702;  
Best Local Similarity 76.6%; Pred. No. 3.8e-33;  
Matches 166; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 213 GGTGGGGGAGAGCCGACTTAACACTAGACGAGTGAACATCATGAGCTTATCTTG 272  
DB 185 GGAGGCTTACACCGGGAGAGCTATTAAAGCCAGTGAACATCATGAGCTTACACAG 244  
QY 273 TGGCAAGAAATCCAGAGCTTCACTTACCGCGGAGACATGAGGCTCACTCCAGCTT 332  
DB 245 TGGCGAAGAGCTTAAATAATTCTTCTTCACTCGCGGAGACACGGGCTCACTCCAGCTT 304  
QY 333 CGAGTGGGCTGCTTACCGGGCTGGTTCCTGTGACAGGTCCTGAAGCCGATCAGCTGT 392  
DB 305 TGAGTGGGCTGCTTACCGAGCTGGTTCCTGTGACAGGTCCTGAAGCTGACAGCTCT 364  
QY 393 CAGACTCACCAGCTTCCGAGAAATGATGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 452  
DB 365 GCAGATCACCAGCTTCCGAGAAATGATGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 424  
QY 453 CCAGCAGTGTACTAG 468  
DB 425 CCAGCAATGTACTAG 440

RESULT 27 689 bp mRNA linear EST 05-AUG-2004  
CD368042 LOCUS  
UI-H-FTI-bkc-a-09-0-UI.81 NCI CGAP FTI Homo sapiens cDNA clone  
DEFINITION  
UI-H-FTI-bkc-a-09-0-UI 3', mRNA sequence.  
ACCESSION  
CD368042.1 GI:31152132  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 689)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 31-139, >LINE2 (matched complement)  
Seq primer: M13 FORWARD  
POLY-A-Tes.

FEATURES  
source  
1..689  
/organism="Homo sapiens"  
/mol\_type="mRNA"

## ORIGIN

Query Match 32.7%; Score 153; DB 6; Length 689;  
Best Local Similarity 100.0%; Pred. No. 3.3e-31;  
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 GGGCTCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTT 375  
DB 685 GGGCTCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTT 626  
QY 376 GAAGCCGATCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTT 435  
DB 625 GAAGCCGATCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTT 566  
QY 436 ATCAGAGCTTCTTCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTT 468  
DB 565 ATCAGAGCTTCTTCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTT 533

RESULT 28 784 bp DNA linear GSS 17-JUN-2003  
CC526753 LOCUS  
CH240\_401P.T7 CHORI-240 Bos taurus genomic clone CH240\_401P,  
DEFINITION  
genomic survey sequence.  
ACCESSION  
CC526753  
VERSION  
CC526753.1 GI:31845041  
KEYWORDS  
GSS.  
SOURCE  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Bovidae; Bovinae; Bos.

REFERENCE  
1 (bases 1 to 784)  
/organism="Bos taurus"  
/mol\_type="DNA"

/db\_xref="taxon:9606"  
/clone="UI-H-FTI-bkc-a-09-0-UI"  
/tissue\_type="Alveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI-CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The RNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The RNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGGCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.  
TAG TISSUE=Human Lung Alveolar Macrophage  
TAG\_LIB=UI-H-FTI  
TAG\_SEQ=GGCATGCGG"

AUTHORS

Holt, R., Scott, J., Yang, G., Barber, S., Smailus, D., Prabh, A., L.,  
Teal, M., Cloutier, A., Lee, D., Ginn, N., Olson, T., Mayo, M.,  
Butterfield, Y., Kirpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,  
Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,  
Schein, J., Marra, M., de Jong, P., Keefe, J. W. and Kappe, S. M.  
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478  
Unpublished (2003)  
Other GSSs: CH240\_401P1.TARBAC3P2

TITLE

Sequencing

The British Columbia Cancer Agency Genome Science Centre  
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6  
Tel: 604-877-6085  
Fax: 604-877-6276

Email: rholtd@bccsc.ca

Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.html). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the  
British Columbia Genome Sciences Centre, Canada.  
Plate: 401 row: P column: 1  
Seq primer: T7

FEATURES

Location/Qualifiers  
1..784

/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_401P1"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 28.0%; Score 131; DB 9; Length 784;  
Best Local Similarity 78.2%; Pred. No. 4.2e-25;  
Matches 169; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

253 ATCATGAGACTTATTTGGTGCAGGAATCCAGAGCTTCACTTACCGGGGGAC 312  
|||  
49 ATCATGAGACTTACCAACAGNGCCGA-GAAGCTTACCTTCACTTACCGGGGGAC 107  
|||  
313 ATGGGGGCTACCTCCAGCTTCGAGTGGGCTTACCGGGGGTTCGTTGACAGGTTG 372  
|||  
108 ACGGGGCTACCTCCAGCTTGAAGTGGCTTACCGAGGCTGTTTCTTTGACAGTGG 167  
|||  
373 CCTGAAGCGATCAGCTGTCACTACCCAGCTTCCGAGATGGTGGCTGAATGCC 432  
|||  
168 CCGAAGCTGACAGGCTCTGAGATCAACCACTCCGAGAGACACGCTGGGACAC 227  
|||  
433 CCCATACAGACTTCTTACTTCCAGCAGTGTACTAG 468  
|||  
228 CCCATCATGACTTCTTACTTCCAGCAATGTGACTAG 263  
|||

RESULT 29

CF116914 501 bp mRNA linear EST 23-JUL-2003  
LOCUS CF116914  
DEFINITION ad97.z1 ad adult sheep skin library Ovis aries CDNA, mRNA sequence.  
ACCESSION CF116914  
VERSION CF116914.1 GI:33179328  
KEYWORDS EST.  
SOURCE Ovis aries (sheep)  
ORGANISM Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

REFERENCE

1 (bases 1 to 501)  
Adelson, D. L., Cam, G. R., Desliya, U. and Franklin, I. R.  
Gene expression in sheep skin and wool (hair)  
Genomics 83 (1), 95-105 (2003)  
CONTACT: Adelson, David L.  
CSIRO Livestock Industries  
306 Carmody Road, St Lucia QLD 4067, Australia  
Tel: +61 7 3214 2700  
Fax: +61 7 3214 2900  
Email: li-enquiries@csiro.au.

FEATURES

Location/Qualifiers  
1..501

/organism="Ovis aries"  
/mol\_type="mRNA"  
/strain="Merino"  
/db\_xref="taxon:9940"  
/sex="male"  
/dev\_stage="Adult"  
/lab\_host="BM25.8"  
/clone\_lib="ad adult sheep skin library"  
/note="Organ: midflank skin; Vector: pTIPlex; Site 1:  
EcoRI; Site 2: XbaI; Arrayed library filters screened by  
hybridization with labeled dinucleotide repeats. First  
strand synthesis XbaI-(dT)15 primed, EcoRI adaptors were  
ligated to cDNA before cloning. EcoRI-NotI-Sall adaptor  
sequence: 5'-AATTGGCGCGGCTGAC GCGCGGCGAGCTG-PQ-5' 5'  
sequencing primer 5' TCCGAGATCTGACAGAC 3' sequencing  
primer 5' TATACGACTCTACTTACG 3' submitted sequences in  
excess of 50 bp after vector and quality clipping (phred  
13) submitted to GenBank."

ORIGIN

Query Match 26.8%; Score 125.2; DB 6; Length 501;  
Best Local Similarity 60.9%; Pred. No. 1.6e-23;  
Matches 240; Conservative 0; Mismatches 148; Indels 6; Gaps 2;

15 GCGCGTGTGCTTCCAGATGAAGACTCCGATTTGAGTGTCTTATCTGATATATACCA 74  
|||  
69 GCGAATAATCTATCATATTAAGAATGACAGAGAGAGCTCTGTACGTAGAGATGGCCA 128  
|||  
75 GCTTACCTGAGAGGCTGATGACAGGAGATCTTAAAGTGAAGATCAGCGTGT 134  
|||  
129 GTTCTGTGGAGATCCGATGACAGCAAA--CTGTATGACAGACCATCTGATACT 185  
|||  
135 CCCCATGTGTGTGATGACAGCTTCCCCCTCATCTCGGTGTCACAGGTGGAAG 194  
|||  
186 CCCCAAGAGACCTGGAACGACCAAGTTCCTTCCTTGGAGGTTCAGAGAGTGA 245  
|||  
195 CCAAGTCTGTATGTGGGTTG---GGCAGAGAGCCGACTTAACTTAACTTAACTTAA 251  
|||  
246 CCGTGTCTGTGATGTGTGAGACAGAGGAGGAGGCTTCCCTGACAGTGAAGATGTGA 305  
|||  
252 CATCATGAGCTCTATCTTGTGCAAGAGATCCAAAGCTTACCTTACCCGGGGA 311  
|||  
306 CATTGAAGACCTGTCAAGAGGTGAGAGAAACACCCGCTTCACTTCTTCCAGAGA 365  
|||  
312 CATGGGCTCACCTTCAGCTTGAAGTGGCTGCTACCCGGGCTGCTCTGACCGGT 371  
|||  
366 CTCAGGCCCGGCTTTCAGGCTGAGGCTGCTGCTGCTGCTGCTCTCTCTGCTC 425  
|||  
372 GCGTGAAGCGATCAGCTGTGACATCAACCCAG 405  
|||  
426 CTTGTGAACCCAGCAGCCCTGCACTTACCAAG 459  
|||

RESULT 30

BY714015 621 bp mRNA linear EST 17-DEC-2002  
LOCUS BY714015  
DEFINITION BY714015 RIKEN full-length enriched, 0 day neonate skin Mus  
musculus CDNA clone 4632413N13 5', mRNA sequence.  
ACCESSION BY714015  
VERSION BY714015.1 GI:27126185

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sclerognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 621)  
Kasakawa, Y., Furuno, M., Kasakawa, T., Adachi, T., Bono, H., Kondo, S.,

**Source**

```

1. .621
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4632413M13"
/sex="mixed"
/tissue_type="skin"
/dev_stage="0 day neonate"
/lab_host="DRI08"
/clone_id="RIKEN full-length enriched, 0 day neonate
skin"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 5'
GAGAGAGAGAGAGATCCAGACGCTCTTTTTTTTTTTTTTTTNN 3', cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence 5' GAGAGAGATTCGTGAGTTATTAATTAATCCCCCCCCCCCC
3'. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I"

```

**ORIGIN**

	Query Match	26.4%	Score 123.6	DB 5	Length 621
	Best Local Similarity	76.6%	Pred. 0.45e-23		
	Matches 164	Conservative 0	Mismatches 49	Indels 1	Gaps 1
QY	1	ATGTCCTGAGTGGGGCGCTGCTCTTCCGATAGAGACTCGGCATTGAAGTGCCTTAT	60		
Db	319	ATGGTCTGTGATGGGGCACATATCTTCCGATAGAGATTCAACTTGAAGTACTGTAT	378		
QY	61	CTGCATATATACGAGCTTCTAGCTGTGAGGGCTGCATGCGAGGAAAGTCATTAAAGTGAA	120		
Db	379	CTGAACAAACACGAGCTGCTGCTGGAGGACCTCAGCCAGCAAGAGTCATTAAAGTGAG	438		
QY	121	GAGATCAGCGTGTGCTCCCATCGGTGGCTGATGCCAGCCTGTCTCCCGTCATCTGGGT	180		
Db	439	GAGATCAGTGTGTCCCAAT- GGGGACCTGATGCCCCCTGTCTCCCTGTCACTCCGGGC	497		
QY	181	GTCGAGGTGGAAGCCAGTGCCTGTCAATGTGGGG	214		
	498	GTTCAAGGAAGAACCCCGCTGCTTATCTTGGGG	531		

## RESULT 31

LOCUS	CD694328	593 bp	mRNA	linear	EST 25-JUN-2003
DEFINITION	EST10851 human nasopharynx Homo sapiens CDNA, mRNA sequence.				

ORGANISM	Homo sapiens (human); Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Cactarihini; Homiidae; Homo. 1 (bases 1 to 593)
REFERENCE	Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
AUTHORS	Zeng, Y.-X.
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL	Unpublished (2003)
COMMENT	Contact: Yixin Zeng

## FEATURES

**Location/Qualifiers**

Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@zsu.edu.cn.  
 Location/Qualifiers

# FEATURES

source

1..593  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="human nasopharynx"  
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

# ORIGIN

Query Match 23.9%; Score 111.8; DB 6; Length 593;  
 Best Local Similarity 59.1%; Pred. No. 8.3e-20;  
 Matches 238; Conservative 0; Mismatches 147; Indels 18; Gaps 2;

24 CTTCCGATGGAAGAGCTGGCATTTGAGTGTATTCGATTAATTAACCACTTCTAGC 83  
 141 CTTCCGATTTGGAGATTTTAACCAAGACCTTCTATCTGAGGAAACCACTAGTTC 200  
 84 TGGAGGGCTGCATGACGAGGAGTCATTAAAGTGAGATCAAGTGTCCCAATCG 143  
 201 TGGATTAATTTGACAGGACCAATATGTCAATTAAGAAAAGATAGATGTGTACCATTTGA 260  
 144 GTGGCTGATGCCAGCTCTCCCGCTCATCTCGGTGTCCAGGGTGGAGGCAATGCTT 203  
 261 GCTCATATGCTC-----TGTCTTGGGAATCCATGAGGGAAGATGTGCTT 305  
 204 GTCATGTGGGGTGT---GGGAGAGCCGACCTTAACACTAGAGCCAGTGAATCATGGA 260  
 306 GTCTCTGTCAAGTCTGTGATGAGACCAAGATCTCCAGCTGGAGGCAATTAATCACTGA 365  
 261 GCTCATATTTGGTGCAGAGAAATCCAAAGCTTCACTTCAACCGGAGGAGATGGAGCT 320  
 366 CCTGAGCGAGAACAGAAACAGAGCAAGGCTTCGCTTCATCCGCTCAGACAGCGGCC 425  
 321 CACCTTCAGCTTTCGATCGGCTGCCCTAACCAGGCTGTCTGTGACCGTCCCTGAAGC 380  
 426 CACCAACGATTTTCGATGTGCGCGCTGCCCGGTGTCTCTGTGACAGCATGGAGAC 485  
 381 CGATCAGCTGTTCAGACTCACCAGCTTCCCGAATGTGTGC 423  
 486 TGAACGCCCCGTACGCTTCAACCAATATGCTTACAGAGGCGTC 528

RESULT 32  
 BX416842 884 bp mRNA linear EST 03-MAY-2004  
 LOCUS BX416842 Homo sapiens PLACENTA Homo sapiens cDNA CS0DE001YA18

DEFINITION 5-PRIME, mRNA sequence.  
 ACCESSION BX416842  
 VERSION BX416842.2 GI:46954039

KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 884)  
 TITLE Li W.B., Gruber C., Jesse J., and Polayes D.  
 JOURNAL Full-length cDNA libraries and normalization  
 COMMENT Unpublished (2001)  
 On May 15, 2003 this sequence version replaced gi:30763662.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.  
 Location/Qualifiers

# FEATURES

source

1..884  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DE001YA18"  
 /tissue\_type="PLACENTA"  
 /clone\_lib="Homo sapiens PLACENTA"  
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

# ORIGIN

Query Match 23.6%; Score 110.6; DB 5; Length 884;  
 Best Local Similarity 58.3%; Pred. No. 1.9e-19;  
 Matches 235; Conservative 3; Mismatches 147; Indels 18; Gaps 2;

24 CTTCCGATGGAAGAGCTGGCATTTGAGTGTATTCGATTAATTAACCACTTCTAGC 83  
 123 CTTCCGATTTGGAGATTTTAACCAAGACCTTCTATCTGAGGAAACCACTAGTTC 182  
 84 TGGAGGGCTGCATGACGAGGAGTCATTAAAGTGAGATCAAGTGTCCCAATCG 143  
 183 CGGATTAATTTGACAGGACCAATATGTCAATTTAAGAAAAGATAGATGTGTACCATTTGA 242  
 144 GTGGCTGATGCCAGCTCTCCCGCTCATCTCGGTGTCCAGGGTGGAGGCAATGCTT 203  
 243 GCTCATATGCTC-----CGCTGTCTTGGGAATCCATGAGGGAAGATGGGCTT 287  
 204 GTCATGTG---GGTGGGAGAGAGCCGACCTTAACACTAGAGCCAGTGAATCATGGA 260  
 288 GCTCTGTGCAAGGCGGAGAGAGACCAAGATCTCAAGCKGAGGAGATTAATCACTGA 347  
 261 GCTCATATTTGGTGCAGAGATCCAAAGCTTCACTTCAACCGGAGGAGATGGAGCT 320  
 348 CCTGAGCGAGAACAGAAAGCAGAGCAAGGCTTCGCTTCATCCGCTCAGACAGTGGCCC 407  
 321 CACCTTCAGCTTTCGATCGGCTGCCCTAACCAGGCTGTCTGTGACCGTCCCTGAAGC 380  
 408 CACCAACGATTTTCGATGTGCGCGCTGCCCGGTGTCTCTGTGACAGCATGGAGAC 467  
 381 CGATCAGCTGTTCAGACTCACCAGCTTCCCGAATGTGTGC 423  
 468 TGAACGCCCCGTACGCTTCAACCAATATGCTTACAGAGGCGTC 510

RESULT 33  
 AY402945 470 bp DNA linear GSS 15-DEC-2003  
 LOCUS AY402945

DEFINITION genomic survey sequence.  
 ACCESSION AY402945  
 VERSION AY402945.1 GI:39758928

KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 470)  
 TITLE Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civejello, D.R., Lu, F., Murphy, B.,  
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Srinisky, J.V.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUMED 14671302  
 REFERENCE 2 (bases 1 to 470)  
 JOURNAL Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,



VERSION B1489807.1 GI:15329035  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 864)  
 AUTHORS NIH-MGC <http://mgi.mci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-rc@mail.nih.gov](mailto:cgabs-rc@mail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Place: LBL/ML1430 row: 9 column: 09  
 High quality sequence stop: 862.  
 Location/Qualifiers  
 1..864  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5172896"  
 /lab\_host="DH10B"  
 /clone\_1ib="NIH MGC 115"  
 /note="Organ: pooled brain, lung, testis; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH MGC Library."

ORIGIN  
 Query Match 23.5%; Score 110.2; DB 3; Length 864;  
 Best Local Similarity 58.8%; Pred. No. 2.5e-19;  
 Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

24 CTTCCGAATGAAGACTCGGCAATGAAGTCTTATCTGCATATATACCAAGCTTTAGC 83  
 144 CTTGAGAACTCTGGAGTTTAAACCAAGAACTTCTATCTGAGGAAACAACAAGTTCG 203  
 84 TGGAGGGCTGCATGACAGGGAAGTCAATTAAGGTGAAGATCAGCTGTGTCCTCAATG 143  
 204 TGGATATCTTGCAAGGACCAAAATGTCAATTAAGAAAGAAATGATGTGTATCCATTA 263  
 144 GTGGCTGATGTCAGAGCTGTCCCGCTCATCTCGGGTGTCAAGGTGGAAGCAGAGCT 203  
 264 GCTCATGCTC-----TGTCTTGGGAATCATGAGGGAAGATGTGCT 308  
 204 GTTCATGTGGGGTG---GGGACAGAGCCGACTTACACTAGAGCCAGTAACATCATGA 260  
 309 GTCTCTGTCTCAAGTCTGTGATGAGACAGACTCCAGCTGAGGAGGAGTTCATCACTGA 368  
 261 GCTCTATCTTGGTGCAGGAATTCAGAGCTTCACTTACACGGCGGGAACATGGGGCT 320  
 369 CCTGAGCGAAGAACAGAAAGAGGACAAAGCGCTTCGCTTCATCCGCTCAGACAGCGGCC 428  
 321 CACCTCAAGCTTGAAGTGGGCTGCTTACCCGGGCTGGTTCCTGTGACGGTGCCTGAAG 380  
 429 CACCAACAATTTTGAATCTGCGCTGCGCCGGTGGTTCCTCTGCAACAGCATGGAAGC 488  
 381 CGATCAGCCTGTGAGACTCACCAAGCTTCCGGAATGTGGC 423  
 489 TGAACAGCCGCTCAGCCTCAATATATGCTGACGAAGGCGTC 531

RESULT 36  
 C619093  
 LOCUS  
 DEFINITION Full-length cDNA clone CSOD1086VA15 of Placenta Cot 25-normalized  
 of Homo sapiens (human).  
 ACCESSION C619093  
 VERSION C619093.1 GI:50499900  
 KEYWORDS HTC; CDSUT\_cDNA  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1581)  
 AUTHORS Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 REMARK Contact: Feng Liang Email: [eliang@lifetech.com](mailto:eliang@lifetech.com) URL:  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
 Faraday Avenue  
 2 (bases 1 to 1581)  
 Genoscope.  
 Direct Submission  
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail: [segreg@genoscope.cns.fr](mailto:segreg@genoscope.cns.fr))  
 - Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 Location/Qualifiers  
 1..1581  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSOD1086VA15"  
 /tissue\_type="Placenta Cot 25-normalized"  
 /plasmid="pCMVSPORT\_6"

ORIGIN  
 Query Match 23.5%; Score 110.2; DB 4; Length 1581;  
 Best Local Similarity 58.8%; Pred. No. 2.8e-19;  
 Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

24 CTTCCGAATGAAGACTCGGCAATGAAGTCTTATCTGCATATATACCAAGCTTTAGC 83  
 48 CTTGAGAACTCTGGAGTTTAAACCAAGAACTTCTATCTGAGGAAACAACAAGTTCG 107  
 84 TGGAGGGCTGCATGACAGGGAAGTCAATTAAGGTGAAGATCAGCTGTGTCCTCAATG 143  
 108 TGGATATCTTGCAAGGACCAAAATGTCAATTAAGAAAGAAATGATGTGTATCCATTA 167  
 144 GTGGCTGATGTCAGAGCTGTCCCGCTCATCTCGGGTGTCAAGGTGGAAGCAGAGCT 203  
 168 GCTCATGCTC-----TGTCTTGGGAATCATGAGGGAAGATGTGCT 212  
 204 GTTCATGTGGGGTG---GGGACAGAGCCGACTTACACTAGAGCCAGTAACATCATGA 260  
 213 GTCTGTGTCTCAAGTCTGTGATGAGACAGACTCCAGCTGAGGAGGAGTTCATCACTGA 272  
 261 GCTCTATCTTGGTGCAGGAATTCAGAGCTTCACTTACACGGCGGGAACATGGGGCT 320  
 273 CCTGAGCGAAGAACAGAAAGAGGACAAAGCGCTTCGCTTCATCCGCTCAGACAGTGGGCC 332  
 321 CACCTCAAGCTTGAAGTGGGCTGCTTACCCGGGCTGGTTCCTGTGACGGTGCCTGAAG 380  
 333 CACCAACAATTTTGAATCTGCGCTGCGCCGGTGGTTCCTCTGCAACAGCATGGAAGC 392  
 381 CGATCAGCCTGTGAGACTCACCAAGCTTCCGGAATGTGGC 423

Db 393 TGACGAGCCGTCAGCTCAACCAATATGCTGAGGAGGCTC 435

RESULT 37  
LOCUS CR616671 1644 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CS0DM013YE17 of Fetal Liver of Homo sapiens (human).  
ACCESSION CR616671  
VERSION CR616671.1 GI:50497478  
KEYWORDS HTC; CNSLT\_CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1644)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1644)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
Location/Qualifiers  
1. .1644  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DM013YE17"  
/issue\_type="Fetal liver"  
/plasmid="pCMVSPORT\_6"

ORIGIN

Query Match 23.5%; Score 110.2; DB 4; Length 1644;  
Best Local Similarity 58.8%; Pred. No. 2.8e-19;  
Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

24 CTTCCGAATGAGAGCTCGGCAATTGAAGTGCTTTATCTGCATTAATACCAAGTTTACG 83  
118 CTTCAAGATCTGGAGATGTTAACCAGAAAGACCTTCTATCTGAGGAACAACCACTTAATTGC 177  
84 TGGAGGGCTGCATGACGAGGAGGTCATTAAGGTGAAGATCAGCGTGTCCCAATCG 143  
178 TGGATCTCTGCAAGGACCAAAATGTCAATTTAGAAGAAAGATAGATGTGGTACCAATGA 237  
144 GTGGCTGATGCCAGCTGTCCCGCTCATCTCGGGTGTCCAGGGTGAAGCAAGTGCCT 203  
238 GCTCATGTCTC-----TGTCTTGGGAATCCATGAGGGAAGATGTGCGCT 282  
204 GTCATGTGGGGTNG---GGGAGAGCGGCACTTAACACTAGAGCCAGTGAACATCATGGA 260  
283 GTCTGTGTCAAGTCTGTGATGATGACACAGATCTCGAGCTGAGAGGCAATTAACTCACTGA 342  
261 GCTTATCTTGTGTCAGGAATTCAGAGCTTCACTTCTTACCGGCGGAGCAATGGGGCT 320  
343 CCGAGCGAGAACAGAAAGAGAGCAAGGCGCTTCGCTTCATCCGCTCAGACAGTGGGCC 402  
321 CACCTTCAGCTTGAAGTCCGCTGCTTACCCGGGCTGTTCCTGTGACAGGTGCTGAAGC 380  
403 CACCAACCAATTTTGAATCTGCGCGCTGCGCCGGGTGGTTCCTCTGACAGCGATGGAAGC 462  
381 CATTACGCTGTGTGAGATCAACCAAGCTTCCGAGATGTGGC 423

Db 463 TGACGAGCCGTCAGCTCAACCAATATGCTGAGGAGGCTC 505

RESULT 38  
LOCUS CR605915 1666 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CS0DE001YA17 of Placenta of Homo sapiens (human).  
ACCESSION CR605915  
VERSION CR605915.1 GI:50486722  
KEYWORDS HTC; CNSLT\_CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1666)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1666)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
Location/Qualifiers  
1. .1666  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DE001YA17"  
/issue\_type="Placenta"  
/plasmid="pCMVSPORT\_6"

ORIGIN

Query Match 23.5%; Score 110.2; DB 4; Length 1666;  
Best Local Similarity 58.8%; Pred. No. 2.8e-19;  
Matches 237; Conservative 0; Mismatches 148; Indels 18; Gaps 2;

24 CTTCCGAATGAGAGCTCGGCAATTGAAGTGCTTTATCTGCATTAATACCAAGTTTACG 83  
123 CTTCAAGATCTGGAGATGTTAACCAGAAAGACCTTCTATCTGAGGAACAACCACTTAATTGC 182  
84 TGGAGGGCTGCATGACGAGGAGGTCATTAAGGTGAAGATCAGCGTGTCCCAATCG 143  
183 TGGATCTCTGCAAGGACCAAAATGTCAATTTAGAAGAAAGATAGATGTGGTACCAATGA 242  
144 GTGGCTGATGCCAGCTGTCCCGCTCATCTCGGGTGTCCAGGGTGAAGCAAGTGCCT 203  
243 GCTCATGTCTC-----TGTCTTGGGAATCCATGAGGGAAGATGTGCGCT 287  
204 GTCATGTGGGGTNG---GGGAGAGCGGCACTTAACACTAGAGCCAGTGAACATCATGGA 260  
288 GTCTGTGTCAAGTCTGTGATGATGACACAGATCTCGAGCTGAGAGGCAATTAACTCACTGA 347  
261 GCTTATCTTGTGTCAGGAATTCAGAGCTTCACTTCTTACCGGCGGAGCAATGGGGCT 320  
348 CCGAGCGAGAACAGAAAGAGAGCAAGGCGCTTCGCTTCATCCGCTCAGACAGTGGGCC 407  
321 CACCTTCAGCTTGAAGTCCGCTGCTTACCCGGGCTGTTCCTGTGACAGGTGCTGAAGC 380  
408 CACCAACCAATTTTGAATCTGCGCGCTGCGCCGGGTGGTTCCTCTGACAGCGATGGAAGC 467

QY 381 CGATAGCCTGTGACACTCACCAGCTTCCCGAGAATGTGGC 423  
 DB 468 TGACACGCCCTGACCTCACCAATATGCTGACGAGGCGTC 510  
 RESULT 39  
 CD468528 735 bp mRNA linear EST 04-JUN-2003  
 LOCUS Leukos\_3\_D10\_g1\_A025 Stimulated peripheral blood leukocytes S3  
 DEFINITION Equus caballus cDNA clone Leukos\_3\_D10\_A025 5', mRNA sequence.  
 ACCESSION CD468528  
 VERSION CD468528.1 GI:31389796  
 KEYWORDS EST  
 SOURCE Equus caballus (horse)  
 ORGANISM Equus caballus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 1 (bases 1 to 735)  
 Vandenplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S.,  
 Moore, J.N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L.H.,  
 An EST database from equine (Equus caballus) stimulated peripheral  
 blood leukocytes  
 Unpublished (2003)  
 JOURNAL Contact: Cordonnier-Pratt MM  
 COMMENT Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmprratt@uga.edu  
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
 the Human Genome Center, University of Tokyo Institute of Medical  
 Science; tissue and RNA were prepared in the Department of Large  
 Animal Medicine, University of Georgia; sequencing done in the  
 Laboratory for Genomics and Bioinformatics, University of Georgia.  
 Sequence ends have been trimmed to exclude vector and regions below  
 phred quality 16. Three-prime sequences are presented as their  
 reverse complement and have been trimmed to exclude polyA.  
 Seq primer: Sugs (CTCTGCTTAAAGCTGCG).  
 Location/Qualifiers  
 1..735  
 /organism="Equus caballus"  
 /mol\_type="mRNA"  
 /strain="Tennessee walking horse"  
 /db\_xref="taxon:9796"  
 /clone="Leukos\_3\_D10\_A025"  
 /sex="female"  
 /tissue\_type="blood"  
 /cell\_type="leukocytes"  
 /lab\_host="DH10B-T1 phage-resistant E. coli"  
 /clone\_lib="Stimulated peripheral blood leukocytes S3"  
 /note="Organ: circulatory system; Vector: pME18S-FL3;  
 Site 1: XhoI; Site 2: XhoI; The library was prepared from  
 polyA+ RNA from equine peripheral blood leukocytes  
 isolated from a healthy adult horse. The leukocytes were  
 stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.  
 Double-stranded cDNA was cloned unidirectionally into  
 different DraIII sites of the pME18S-FL3 vector (5-prime  
 DraIII site is CACTGTGTG, 3-prime DraIII site is  
 CACCATGTG). XhoI excises the cDNA insert."

## ORIGIN

Query Match 23.3%; Score 109; DB 6; Length 735;  
 Best Local Similarity 57.0%; Pred. No. 5.2e-19;  
 Matches 249; Conservative 0; Mismatches 170; Indels 18; Gaps 2;

QY 24 CTTCCAGTAAGAGACTCGGCAATTGAAGCGCTTTATCGCATATACAGGCTTACG 83  
 DB 141 CTTCCAGTAATTTGGAGATTATACCAAGAACCTTCTACATAGAGAAATACCAACTAGTGC 200  
 QY 84 TGGAGGGCGGTGCATATCAGGAGAGTCAATTAAGGTGAAGATCAGCGTGTGCCCAATCG 143  
 DB 201 TGGATATCTTGCAGAAATCAAAATCTAAATTAACAAGAGAAATATGTTGTGTGCCCATTTGA 260

QY 144 GTGGCTGATGCAAGCCGTGTCGCCCGTATCTGGGTGTCCAGGGTGAAGCCAGTGCCT 203  
 DB 261 G-----CTGATGCTCTATTCTCTGGAGACTCATGGAGAGAGCTGTGCT 305  
 QY 204 GTCATGTG---GGTGGGGCAGAGCCGACTCTTAACACTAGACCAATGAACTATGGA 260  
 DB 306 GGCCTGTGTAAGTCTGTGATGATGAGTTAGTTCAAATTGAGGAGAGTAAACATACATGA 365  
 QY 261 GCTCATTTTGGTGGCAAGAAATCCAGAGCTTCACTTCAACCGCGGAGCATGGGGCT 320  
 DB 366 CCTGAGCAAGAACAAAGAGAGAGAACAGCGCTTCACTTCAATCCGCTCAAAACATGGGCC 425  
 QY 321 CACCTCGAGCTTGAAGTGGCGCTGACCTACCGGAGCTGTTCCTGTGTCAGAGTGCCTGAAGC 380  
 DB 426 CACCAACGAGCTTCAGAGTCTGCGGCTGCTGCGCTGTGCTTCTCTCAACGCGCGGAGGCT 485  
 QY 381 CGATCAGCCTGTGACACTCACCAGCTTCCGAGAAATGTGGCTGAAATGCCCATCAG 440  
 DB 486 AGACGGCCTGTGACGCTCACCAACAGCCCTCAGAAAGAGGTACACGAGCCCTGTAAAC 545  
 QY 441 AGACTTCTACTTCCAGC 457  
 DB 546 AGGACTCTGTCTCCAGC 562

RESULT 40  
 LOCUS CV027812 572 bp mRNA linear EST 20-AUG-2004  
 DEFINITION 6164 Full Length cDNA from the Mammalian Gene Collection Homo

ACCESSION CV027812  
 VERSION CV027812  
 KEYWORDS sapiens cDNA 5' similar to BC009745, mRNA sequence.  
 EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

1 (bases 1 to 572)  
 Rual, J.-F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,  
 Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,  
 Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,  
 Simmons, B., Segueria, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,  
 Vandenhaute, J., Cusick, M.E., Albaladejo, J.S., Hill, D.E. and Vidal, M.  
 Human ORFeome Version 1.1: a Platform for Reverse Proteomics  
 Genome Res. (2004) In press

JOURNAL COMMENT  
 Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739  
 Email: Marc\_Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF  
 results from a PCR reaction using an MGC full-length cDNA as  
 template DNA and ORF specific primers  
 PCR Primers  
 FORWARD: ATGGCTTTAGAGACATCTG  
 BACKWARD: TACTCGTCTCTCTGAGATGAA  
 Insert Length: 572 Std Error: 28.00  
 Plate: 11002 row: 07 column: G  
 Seq primer: ACTGGCGGTGTTTACACAGCTGTAAGTGGGAAAC  
 High quality sequence start: 100  
 High quality sequence stop: 571  
 POLYA=NO.

FEATURES  
 source Location/Qualifiers  
 1..572  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="mixed"  
 /clone\_lib="Full Length cDNA from the Mammalian Gene



Collection"  
/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team. Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(126), 16899-16903"

## ORIGIN

Query Match 23.2%; Score 108.6; DB 7; Length 572;  
Best Local Similarity 58.6%; Pred. No. 6.3e-19;  
Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

24 CTTCGAAATGAGAGCTCGGCAATGAGAGTCTTATCTGCAATTAATACAGCTTTAGC 83  
|||||  
57 CTTCGAAATCTGGAGATGTTAACCAGAACCTTCTATCTGAGAGAACCACTAGTTGC 116  
|||||  
84 TGGAGGGCTGATGACAGGAGAGTCAATTAAGGTGAAGATCAGCGTCCCAATCG 143  
|||||  
117 CGGATACCTTGCAAGAGCAAAATGTCAATTAGAAAGAAAGATGATGTGATCCATTGA 176  
|||||  
144 GTGGCTGATGACAGCTCTCCCGCTCATCTCGGTGTCCAGGGTGAAGCCAGTGCCT 203  
|||||  
177 GCCTCATGCTC-----TGTTCTTGGGAATCCATGAGGAGGAAGATGTGCTT 221  
|||||  
204 GTCATGTGGGGT-----GGCAGAGCCGCACTTAACATAGAGCCAGTGAACATCTGA 260  
|||||  
222 GTCTGTGTCAAGTGTGATGATGACGACAGCTCCAGCTGAGGAGGAGTAACTCATGA 281  
|||||  
261 GCTTATCTTGGTGCAGAAATCCAGAGCTTCACTTACCGGCGGAGACATGGGGCT 320  
|||||  
282 CTTGAGCGGAGAACAGAAACAGAGAGCGCTTCGCTTATCCGCTCAGACAGATGGCCC 341  
|||||  
321 CACTTCAGCTTGAAGTGGGCTGCTTACCGGGCTGTCTGTGACAGCGTCCCTGAAGC 380  
|||||  
342 CACCAACAGTTTGAAGTGTGCGCGCTGCGCGGTTGTCTCTGTGACAGCATGGAGC 401  
|||||  
361 CGATCAGCTGTGACAGCTACCCAGCTTCCCGAGATGTGGC 423  
|||||  
402 TGACCAAGCCGTCACGCTCACCATAATGTCTGACGAGAGCGTC 444  
|||||

RESULT 41  
BX424058 757 bp mRNA linear EST 01-MAY-2004  
LOCUS BX424058 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE001YA17  
DEFINITION 5-PRIME, mRNA sequence.  
ACCESSION BX424058  
VERSION BX424058.2 GI:46928937  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 757)  
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 13, 2003 this sequence version replaced gi:30647665.  
Contact: Genoscope

Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 138.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CS1DE001ZA06QPlac=138.f.

## FEATURES

source

Location/Qualifiers

1. 757  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DE001YA17"  
/issue\_type="PLACENTA"  
/clone\_lib="Homo sapiens PLACENTA"  
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

## ORIGIN

Query Match 23.2%; Score 108.6; DB 5; Length 757;  
Best Local Similarity 58.6%; Pred. No. 6.7e-19;  
Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

24 CTTCGAAATGAGAGCTCGGCAATGAGAGTCTTATCTGCAATTAATACAGCTTTAGC 83  
|||||  
123 CTTCGAAATCTGGAGATGTTAACCAGAACCTTCTATCTGAGAGAACCACTAGTTGC 182  
|||||  
84 TGGAGGGCTGATGACAGGAGAGTCAATTAAGGTGAAGATCAGCGTCCCAATCG 143  
|||||  
183 CGGATACCTTGCAAGAGCAAAATGTCAATTAGAAAGAAAGATGATGTGATCCATTGA 242  
|||||  
144 GTGGCTGATGACAGCTCTCCCGCTCATCTCGGTGTCCAGGGTGAAGCCAGTGCCT 203  
|||||  
243 GCCTCATGCTC-----TGTTCTTGGGAATCCATGAGGAGGAAGATGTGCTT 287  
|||||  
204 GTCATGTGGGGT-----GGCAGAGCCGCACTTAACATAGAGCCAGTGAACATCTGA 260  
|||||  
288 GTCTGTGTCAAGTGTGATGATGACGACAGCTCCAGCTGAGGAGGAGTAACTCATGA 347  
|||||  
261 GCTTATCTTGGTGCAGAAATCCAGAGCTTCACTTACCGGCGGAGACATGGGGCT 320  
|||||  
348 CTTGAGCGGAGAACAGAAACAGAGAGCGCTTCGCTTATCCGCTCAGACAGATGGCCC 407  
|||||  
321 CACTTCAGCTTGAAGTGGGCTGCTTACCGGGCTGTCTGTGACAGCGTCCCTGAAGC 380  
|||||  
408 CACCAACAGTTTGAAGTGTGCGCGCTGCGCGGTTGTCTCTGTGACAGCATGGAGC 467  
|||||  
361 CGATCAGCTGTGACAGCTACCCAGCTTCCCGAGATGTGGC 423  
|||||  
468 TGACCAAGCCGTCACGCTCACCATAATGTCTGACGAGAGCGTC 510  
|||||

RESULT 42  
BX406656 932 bp mRNA linear EST 01-MAY-2004  
LOCUS BX406656 Homo sapiens FETAL LIVER Homo sapiens cDNA clone  
DEFINITION CS0DM013YE17 5-PRIME, mRNA sequence.  
ACCESSION BX406656  
VERSION BX406656.2 GI:46926367  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 932)  
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 13, 2003 this sequence version replaced gi:30639467.  
Contact: Genoscope

Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1388.f. For more information about this cluster, see <http://www.genoscope.cns.fr/cdna7a?c=50AM013AC09QPl&c=1388.f>.

## FEATURES

source

Location/Qualifiers  
1..932  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODM013YE17"  
/issue\_type="FETAL LIVER"  
/dev\_stage="fetal"  
/clone\_lib="Homo sapiens FETAL LIVER"  
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

## ORIGIN

Query Match 23.2%; Score 108.6; DB 5; Length 932;  
Best Local Similarity 58.6%; Pred. No. 7e-19;

Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

```

24 CTTCCGAATGAAAGACTGGCATTGAAGTCTTATCTGCATTAATTAACCACTTCTAGC 83
118 CTTCAGAATCTGGAGTGTAAACCAAGACCTTCTATCTGAGAAACAACTAGTGTGC 177
84 TGGAGGGCTGATGACGAGGAGATCAATTAAGTGAAGATCAGCGTGTCCCAATCG 143
178 CGGATATCTTGACAGACCAATGTCAATTTAGAAAGAAAGATGATGTGTACCATTTGA 237
144 GTGGCTGATGTCAGACCTGTCTCCCGCTCATCTGGGTGTCAGGGTGAAGCCAGTGCCT 203
238 GCGTCATGTCTC-----TGTTCTTGGGAATCCATGAGGAGGAAATGTGCTT 282
204 GTCAATGTGGGGT---GGGACAGAGCCGACTCTTAACACTAGAGCCAGTGAATCATGGA 260
283 GTCTGTGTCAAGTCTGTGATGACACAGACTCCAGCTGAGAGGACATTAACTACTGA 342
261 GCTCTATCTTGGTGCAGGAATCCAAAGACTTCACTTCAACCGCGGAGCATGGGGCT 320
343 CTTGAGCGGAGAACAGAAACAGAGAGGCTTCCGCTTATCCGCTCAGACAGTGGGCC 402
321 CACCTTCAGCTTGAAGTGGCTGCTTACCCGGGGCTGTCTGTGACGCGTGCCTGAAGC 380
403 CACCAACAGTTTGAAGTGTGCGCGCTGCCCCGGTTGGTTCCTGTGACAGCATGGAAAGC 462
381 CGATCAGCTGTGACACTCAACCCAGCTTCCGAGAAATGGTGGC 423
463 TGACCAGCCCGTCAAGCTTCAACCAATATGCTTGAAGAGCGTCT 505

```

## RESULT 43

BE563703 938 bp mRNA linear EST 15-AUG-2000  
LOCUS 60135333F1 NIH\_MGC\_39 Homo sapiens cDNA clone IMAGE:3689284 5',  
DEFINITION mRNA sequence.  
ACCESSION BE563703  
VERSION BE563703.1 GI:9807423  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Homosapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 938)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
Unpublished (1999)  
Contact: Robert Strausberg, Ph. D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: L1CM383 row: n column: 05  
High quality sequence stop: 764.

## FEATURES

source

Location/Qualifiers  
1..938  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3689284"  
/issue\_type="adenocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_39"  
/note="Organ: pancreas; Vector: pOTB7, Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G) library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 23.2%; Score 108.6; DB 2; Length 938;  
Best Local Similarity 58.6%; Pred. No. 7e-19;

Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

```

24 CTTCCGAATGAAAGACTGGCATTGAAGTCTTATCTGCATTAATTAACCACTTCTAGC 83
67 CTTCAGAATCTGGAGTGTAAACCAAGACCTTCTATCTGAGAAACAACTAGTGTGC 126
84 TGGAGGGCTGATGACGAGGAGATCAATTAAGTGAAGATCAGCGTGTCCCAATCG 143
127 CGGATATCTTGACAGACCAATGTCAATTTAGAAAGAAAGATGATGTGTACCATTTGA 186
144 GTGGCTGATGTCAGACCTGTCTCCCGCTCATCTGGGTGTCAGGGTGAAGCCAGTGCCT 203
187 GCGTCATGTCTC-----TGTTCTTGGGAATCCATGAGGAGGAAATGTGCTT 231
204 GTCAATGTGGGGT---GGGACAGAGCCGACTCTTAACACTAGAGCCAGTGAATCATGGA 260
222 GTCTGTGTCAAGTCTGTGATGACACAGACTCCAGCTGAGAGGACATTAACTACTGA 291
261 GCTCTATCTTGGTGCAGGAATCCAAAGACTTCACTTCAACCGCGGAGCATGGGGCT 320
292 CTTGAGCGGAGAACAGAAACAGAGAGGCTTCCGCTTATCCGCTCAGACAGTGGGCC 351
321 CACCTTCAGCTTGAAGTGGCTGCTTACCCGGGGCTGTCTGTGACGCGTGCCTGAAGC 380
352 CACCAACAGTTTGAAGTGTGCGCGCTGCCCCGGTTGGTTCCTGTGACAGCATGGAAAGC 411
381 CGATCAGCTGTGACACTCAACCCAGCTTCCGAGAAATGGTGGC 423
412 TGACCAGCCCGTCAAGCTTCAACCAATATGCTTGAAGAGCGTCT 454

```

## RESULT 44

BM009048 955 bp mRNA linear EST 30-OCT-2001  
LOCUS 603618892F1 NIH\_MGC\_39 Homo sapiens cDNA clone IMAGE:5422918 5',  
DEFINITION mRNA sequence.  
ACCESSION BM009048  
VERSION BM009048.1 GI:16523402  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Homosapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE  
1 (bases 1 to 955)  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Homidae; Homo.  
1 (bases 1 to 955)  
NIH-MGC <http://mgs.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: L1CM1881 row: h column: 23  
High quality sequence stop: 792.

FEATURES  
source  
1. 955  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5422918"  
/issue\_type="adenocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 39"  
/note="Organ: pancreas; Vector: pORF7; Site\_1: XhoI;  
Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed  
by Ling Hong in the laboratory of Gerald M. Rubin  
(University of California, Berkeley) using ZAP-CDNA  
synthesis kit (Stratagene) and Superscript II RT (Life  
Technologies)."

ORIGIN  
Query Match 23.2%; Score 108.6; DB 3; Length 955;  
Best Local Similarity 58.6%; Pred. No. 7e-19;  
Matches 236; Conservative 0; Mismatches 149; Indels 18; Gaps 2;

```

QY 24 CTTCCGAATGAAGACTCGGCATTTGAAGTCTTTATCTGCATATATACCACTTCTTAC 83
DB 92 CTTTCAAGATCTGGAGTGTAAACCAAGACCTTCTATCTGAGGAAACCAACTAGTTGC 151
QY 84 TGGAGGGCGCATGACGAGGAGTCAATTAAGTGAAGATCAGGTCGTCCTCCCAATG 143
DB 152 CGGATACCTTGCAAGGACCAATGTCAATTTAAGAAAGAAATGATGTGTACCACTTGA 211
QY 144 GTGGCTGATGTCAGGCTGTCCCGTCATCTCGGCTGTGTCAGGGTGAAGCCAGTGCCT 203
DB 212 GCTCATGTCT-----TGTCTTGGGAATTCATGAGGAAAGATGTGCT 256
QY 204 GTCATGTGGGGTG---GGCAGAGCCGACTTAAACCTAAGACCAAGCAATCATGGA 260
DB 257 GTCTGTGTCAAGTCTGTGATGAGACAGACTCCAGCTGAGGACGAGTTAAATCATCTGA 316
QY 261 GCTCATCTGTGTCGAAGGAATCCAAGAGCTTCACTTACCGCGGAGCAATGGGCT 320
DB 317 CTTGAGCGAAGAACAGAAAGACAGACAGGCTTCCGCTTATCCGCTCAGACAGTGGCC 376
QY 321 CACTTCAGACTTGAAGTGGCTGCTTACCCGGGCTGTTCCTGTGACAGGTCCTGAAGC 380
DB 377 CACCAACAGATTGATGTGCGCGCTGCGCGCTGCGCTGCTTCTGTGACAGCATGGAAGC 436
QY 381 CGATCAGCTGTGACATCAACCACTTCCGGAATGTGGC 423
DB 437 TGACCAGCCCTGACGCTCACCATAATGTGCTGACGAAGGCGTC 479

```

RESULT 45  
AL540334 898 bp mRNA linear EST 24-MAR-2004  
LOCUS AL540334 Homo sapiens PLACENTA Homo sapiens CDNA clone CS0DE001YA17  
DEFINITION 5-PRIME, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AL540334  
AL540334.3 GI:45715958  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
1 (bases 1 to 898)  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Li, W.B., Gruber, C., Jesse, J. and Polyes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:30543383.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 1388.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?e=CS0DE001AA09P1ec=1388.f>.

FEATURES  
source  
1. 898  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DE001YA17"  
/issue\_type="PLACENTA"  
/clone\_lib="Homo sapiens PLACENTA"  
/note="Vector: pCMVSPORT\_6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

ORIGIN  
Query Match 23.1%; Score 108.2; DB 1; Length 898;  
Best Local Similarity 58.3%; Pred. No. 9e-19;  
Matches 225; Conservative 1; Mismatches 149; Indels 18; Gaps 2;

```

QY 24 CTTCCGAATGAAGACTCGGCATTTGAAGTCTTTATCTGCATATATACCACTTCTTAC 83
DB 123 CTTTCAAGATCTGGAGTGTAAACCAAGACCTTCTATCTGAGGAAACCAACTAGTTGC 182
QY 84 TGGAGGGCGCATGACGAGGAGTCAATTAAGTGAAGATCAGGTCGTCCTCCCAATG 143
DB 183 CGGATACCTTGCAAGGACCAATGTCAATTTAAGAAAGAAATGATGTGTACCACTTGA 242
QY 144 GTGGCTGATGTCAGGCTGTCCCGTCATCTCGGCTGTGTCAGGGTGAAGCCAGTGCCT 203
DB 243 GCTCATGTCT-----TGTCTTGGGAATTCATGAGGAAAGATGTGCT 287
QY 204 GTCATGTGGGGTG---GGCAGAGCCGACTTAAACCTAAGACCAAGCAATCATGGA 260
DB 288 GTCTGTGTCAAGTCTGTGATGAGACAGACTCCAGCTGAGGACGAGTTAAATCATCTGA 347
QY 261 GCTCATCTGTGTCGAAGGAATCCAAGAGCTTCACTTACCGCGGAGCAATGGGCT 320
DB 348 CTTGAGCGAAGAACAGAAAGACAGACAGGCTTCCGCTTATCCGCTCAGACAGTGGCC 407
QY 321 CACTTCAGACTTGAAGTGGCTGCTTACCCGGGCTGTTCCTGTGACAGGTCCTGAAGC 380
DB 408 CACCAACAGATTGATGTGCGCGCTGCGCGCTGCGCTGCTTCTGTGACAGCATGGAAGC 467
QY 381 CGATCAGCTGTGACATCAACCACTTCCGGAATGTGGC 423
DB 468 TGACCAGCCCTGACGCTCACCATAATGTGCTGACGAAGGCGTC 510

```

RESULT 46  
AL554778 1069 bp mRNA linear EST 30-MAR-2004  
LOCUS AL554778 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0D1066YA15 5-PRIME, mRNA sequence.  
ACCESSION AL554778  
VERSION AL554778.3 GI:45859528  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 1069)  
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31276588.  
COMMENT Contact: Genoscope - Centre National de Sequencage  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
1388.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CS0D1066YA15&P1c=1388.f.  
FEATURES  
source  
1..1069  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1066YA15"  
/issue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 23.1%; Score 108.2; DB 1; Length 1069;  
Best Local Similarity 58.3%; Pred. No. 9.3e-19;  
Matches 225; Conservative 1; Mismatches 149; Indels 18; Gaps 2;  
24 CTTCCGAATGAGAGACTCGCATTGAAGGCTTATTCGCAATTAATACAGCTTCTAGC 83  
|||||  
48 CTTCAAAATCTGGAGATTTAACGAAGACCTTCTATCTGAGAACCAACCACTTATGTC 107  
|||||  
84 TGGAGGGCTGATGATGAGGAGGAGTAAAGGTGAAGATCAGCGTGTCCCAATCG 143  
|||||  
108 CGGATACTTGCAGAGCAAAATTCATTTAGAAAGAAAGATAGATGTGGTACCATTA 167  
|||||  
144 GTGGCTGATGATCCAGCTGTCCCGCTCATCTGGGTGTCAGAGGTGAAGCAAGTCCCT 203  
|||||  
168 GCCTCATGTCTC-----TGTCTTGGGAATCCATGAGGGAGATGTGCTT 212  
|||||  
204 GTCATGTGGGGT---GGGAGAGGCGCACTTAACACTAGAGCAAGTGAACATCATGA 260  
|||||  
213 GTCTGTGTCAATCTGTGTATAGACACAGCTTCAGCTGGAGCGATTAACATCACTGA 272  
|||||  
261 GCTCTATCTTGTGCAAGATCAAGAGCTTCACTTCTACCGGCGGAGCAATGGAGCT 320  
|||||  
273 CTTGAGGAGAAACAGAAAGAGAGCAAGCGCTTGCCTTATCGCTCAAGACGTGGCCC 332  
|||||  
321 CACCTTCAGCTTGAAGTGGCTGCTTACCCGGCGGTGTTCTGTGCAAGGTGCTTAAGC 380  
|||||  
333 CACCAACAGTTTGAAGTGTGCTGCGCTGCGCGGTGTTCTGTGCAAGCGATGAGAGC 392  
|||||  
381 CGATCAGCTGTGATGATCAACCAAGCTTCCGAGAAATGTGGC 423  
|||||

DB 393 TGACCAAGCCCTCAGCTCAACCAATATGCTGAGAGAGCGCTC 435  
|||||  
RESULT 47  
BM818991 403 bp mRNA linear EST 06-MAR-2002  
LOCUS BM818991  
DEFINITION K-EST0086744 S20T665307 Homo sapiens cDNA clone S20T665307-5-D12  
5' mRNA sequence.  
ACCESSION BM818991  
VERSION BM818991.1 GI:19175404  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 403)  
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished (2002)  
COMMENT TITLE  
JOURNAL  
CONTACT Genome Research Center  
Genome Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kr.ibm.re.kr  
Plate: 5 row: D column: 12  
High quality sequence stop: 403.  
FEATURES  
source  
1..403  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S20T665307-5-D12"  
/sex="M"  
/lab\_host="Top10F"  
/clone\_lib="S20T665307"  
/note="Organ: Stomach; Vector: pCNS; Site: 1: EcoRI;  
Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tobacco acid pyrophosphatase (TAP). The decapped  
cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transfection of  
competent cells E. coli Top10F by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

ORIGIN  
Query Match 22.9%; Score 107; DB 3; Length 403;  
Best Local Similarity 59.6%; Pred. No. 1.6e-18;  
Matches 226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;  
48 GAAGTGTCTTATCTGCAATTAATTAACAGCTTCTAGCTGAGGCGTGCATGAGGAAGT 107  
|||||  
21 GAAGACCTTCTATCTGAGGAACAACTAGTGTGATTAATTCAAGAGCAAAATGT 80  
|||||  
108 CATTAAGGGAAGAGATCAGCGTGTGCCAATCGGTGGCTGATGCCAGCTGTCCCC 167  
|||||  
81 CAATTTAGAAAGAAATAGATGTGTATCCATTTGAGCCTCATGCTC----- 127  
|||||  
168 CGTATCTGTGGGTGTCAGAGGTGAAGCAAGTCCCTGTCAATGTG---GGTGGGAGAGA 224  
|||||

Db 128 --TGTTCTTGGGAATCCATGAGGGAAGATGTCCTGCTGTGCAAGTCTGTATGA 185  
QY 225 GCGCACTTAACACTGAGCGAGTGAACATCATGAGCTTATCTTGTGTGCCAAGATC 284  
Db 186 GACCAACTTCAGCTGAGGCACTTAACATCACTGACTGAGGAGAAACAGAAAGAGGA 245  
QY 285 CAAGAGCTTCACCTTCTACCGCGGAGCATGAGGAGTCACTCCAGCTTCAGTCCGCTGC 344  
Db 246 CAAGGCTTCGCTTATCCGCTCAGACAGCGGCCACACCAAGTTTGAAGTCTGCGCG 305  
QY 345 CTACCCGGGCTGTTCTCTGTGACAGGCTGCTGAAGCCGATCAGCTGTCACTCAACCA 404  
Db 306 CTGCCCCGGTGTGTTCTCTGTGACAGGATGAGAAAGTGAACAGCCGCTGAGCTCAACAA 365  
QY 405 GCTTCCCGAAGATGTGGC 423  
Db 366 TATGCTTGAAGAGGCGTC 384

RESULT 48  
LOCUS BG288796 640 bp mRNA linear EST 21-FEB-2001  
DEFINITION BG288796 602388126F1 NIH\_MGC\_93 Homo sapiens cDNA IMAGE:4516927 5',  
mRNA sequence.  
ACCESSION BG288796  
VERSION BG288796.1 GI:13043994  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 640)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgarbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Place: LLM10409 row: c column: 08  
High quality sequence stop: 635.  
Location/Qualifiers  
1..640  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4516927"  
/tissue\_type="transitional cell papilloma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_93"  
/note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NCI;  
Site 2: Sail; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.7 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC library."

FEATURES  
source  
Query Match 22.9%; Score 107; DB 2; Length 640;  
Best Local Similarity 59.6%; Pred. No. 1.8e-18;  
Matches 226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;  
ORIGIN  
1..640  
Query Match 22.9%; Score 107; DB 2; Length 640;  
Best Local Similarity 59.6%; Pred. No. 1.8e-18;  
Matches 226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;  
ORIGIN

Db 62 CAATTAGAAAGAAAGATGATGTGTACCATTCATGAGCTCATGCTC----- 108  
QY 168 CGTATCTCTGGGTGTCCAGGATGAAAGCCAGTGTCTGTCAATGTG---GCTGGGAGGA 224  
Db 109 --TGTTCTTGGGAATCCATGAGGGAAGATGTCCTGCTGTGCAAGTCTGTATGA 166  
QY 225 GCGCACTTAACACTGAGCGAGTGAACATCATGAGCTTATCTTGTGTGCCAAGATC 284  
Db 167 GACCAACTTCAGCTGAGGCACTTAACATCACTGACTGAGGAGAAACAGAAAGAGGA 226  
QY 285 CAAGAGCTTCACCTTCTACCGCGGAGCATGAGGAGTCACTCCAGCTTCAGTCCGCTGC 344  
Db 227 CAAGGCTTCGCTTATCCGCTCAGACAGCGGCCACACCAAGTTTGAAGTCTGCGCG 286  
QY 345 CTACCCGGGCTGTTCTCTGTGACAGGCTGCTGAAGCCGATCAGCTGTCACTCAACCA 404  
Db 287 CTGCCCCGGTGTGTTCTCTGTGACAGGATGAGAAAGTGAACAGCCGCTGAGCTCAACAA 346  
QY 405 GCTTCCCGAAGATGTGGC 423  
Db 347 TATGCTTGAAGAGGCGTC 365

RESULT 49  
LOCUS BG987216 120 bp mRNA linear EST 13-JUN-2001  
DEFINITION BG987216 MR2-HT1161-050101-004-c12\_1 HT1161 Homo sapiens cDNA, mRNA  
sequence.  
ACCESSION BG987216  
VERSION BG987216.1 GI:14391286  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 120)  
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Coستا, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the RAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
([http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR2&c2=MR2-HT1161-050101-004-c12\\_1&t3=2001-01-05&t4=1](http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR2&c2=MR2-HT1161-050101-004-c12_1&t3=2001-01-05&t4=1))  
Seq primer: puc 18 forward  
High quality sequence stop: 84.  
Location/Qualifiers  
1..120  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="HT1161"  
/note="Organ: head\_neck; Vector: puc18; Site 1: Smat;  
Site 2: Smat; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of

FEATURES  
source  
Query Match 22.9%; Score 107; DB 2; Length 640;  
Best Local Similarity 59.6%; Pred. No. 1.8e-18;  
Matches 226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;  
ORIGIN  
1..640  
Query Match 22.9%; Score 107; DB 2; Length 640;  
Best Local Similarity 59.6%; Pred. No. 1.8e-18;  
Matches 226; Conservative 0; Mismatches 135; Indels 18; Gaps 2;  
ORIGIN

QY 48 GAAGGCTTATTCGATATTAACAGCTTCTAGCTGAGGCGCTGATGAGGGAAGGT 107  
Db 2 GAAGACCTTCTATCTGAGAAACACCACTAGTGTGATCTTGTGCAAGACCAATAT 61  
QY 108 CATTAAGGTGAAGATCAGCGGTGTCCCAATCGGTGCTGATGCGAGCTGTCCCC 167

ORIGIN

tissue mRNA and cDNA amplification were performed under low stringency conditions."

Query Match 22.2%; Score 103.8; DB 2; Length 120;  
Best Local Similarity 96.7%; Pred. No. 9.9e-18;  
Matches 116; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 105 GGTCAATTAAGGTGAAGATCAGCGTGTCCCAATCGGTGGCTGATG-CCAGCTGT 163  
DB 1 GGTCAATTAAGGTGAAGATCAGCGTGTCCCAATCGGTGGCTGATG-CCAGCTGT 60  
QY 164 CCCCCGTATCTGGGTGTCCAGGTGGAAGCCAGTCTGTCAATGCGGTGGGCGCAGG 223  
DB 61 CCCCCGTATCTGGGTGTCCAGGTGGAAGCCAGTCTGTCAATGCGGTGGGCGCAGG 120

RESULT 50  
DQ043278

LOCUS DQ043278 435 bp DNA linear GSS 02-JUN-2005  
DEFINITION Homo sapiens IL1F10 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION DQ043278  
VERSION DQ043278.1 GI:66894493

KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
AUTHORS

TITLE

JOURNAL PubMed  
PUBMED 15869325  
2 (bases 1 to 435)

REFERENCE  
AUTHORS

Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,  
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civeello, D.,  
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.  
A Scan for Positively Selected Genes in the Genomes of Humans and  
Chimpanzees  
(e) PLoS Biol. 3 (6), E170 (2005)

TITLE  
JOURNAL

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment. Translation starts at the beginning of  
alignment.

FEATURES  
Source 1..435  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="2"  
<1..>435  
/gene="IL1F10"  
/locus\_tag="HC10058"

ORIGIN

Query Match 22.2%; Score 103.8; DB 11; Length 435;  
Best Local Similarity 62.2%; Pred. No. 1.3e-17;  
Matches 181; Conservative 0; Mismatches 107; Indels 3; Gaps 1;

QY 118 GAAGATCAGCGTGTCCCAATCGGTGCTGATGCCAGCTGTCCCGCTCATCTTG 177  
DB 94 GAGAAATCTGCTACTTCTTAACAAGGCTTGCCCGCACCAAGGTCCCATTTTCTTG 153

QY 178 GGATTCAGGTTGAAGCCAGTGTCTGTATGTGGGGT---GGGAGAGCCGACTCTA 234  
DB 154 GGGATTCAGGAGGAGCGCTGTCTGTGTGTGAACAGAGAGGGGCTTCCCTTA 213

QY 235 ACACTAGAGCACTGAACATCATGAGCTTATCTTGTGCAAGGATCCAGAGCTTC 294  
DB 235 ACACTAGAGCACTGAACATCATGAGCTTATCTTGTGCAAGGATCCAGAGCTTC 294

DB 214 CAGCTGAGAGATGTGAACATTGAGGAAGTGTGGAAGGCGCACAGCTTC 273  
QY 295 ACCTTCTACCGGCGGAGACATGGGCTCACTCCAGCTTCGAGTGGCTGCTAACCGGGG 354  
DB 274 ACCTTCTTCCAGACAGCACTCAGGCTCCGCTTCAAGGCTTGAGGCTGCTGGCTGGC 333  
QY 355 TGGTTCCTGTGACAGGTGCTGGAAGCCGATGAGCTGTCAAGCTCACCAG 405  
DB 334 TGGTTCCTGTGTGGCCCGGCAAGACCCAGCAGCTCAGTACAGCTTACCAAG 384

Search completed: January 27, 2006, 21:51:48  
Job time : 3090 secs